
M P S R E H
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 20 15:17:56 2000: MasPar time 5.15 Seconds
Tabular output not generated. 600.911 Million cell updates/sec

Title: >US-09-150-947-12
Description: (1-239) from US09150947.pep
Perfect Score: 1763
Sequence: 1 ESQPPDKPELHKSSKFTGL.....NKNWDSKDVKIEVYLTTRKK 239

Scoring table:
PAM 150
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PC9_COMB 4:backfiles1

Statistics: Mean 30.280; Variance 145.353; scale 0.208

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1760	99.8	255	1	US-08-446- Sequence 2, Applicatio	1.55e-143
2	1760	99.8	255	2	US-08-580- Sequence 2, Applicatio	1.55e-143
3	375	21.3	233	1	US-08-446- Sequence 4, Applicatio	9.01e-22
4	375	21.3	233	2	US-08-580- Sequence 4, Applicatio	9.01e-22
5	201	11.4	27	2	US-08-876- Sequence 9, Applicatio	1.93e-07
6	201	11.4	27	1	US-08-165- Sequence 9, Applicatio	1.93e-07
7	196	11.1	27	1	US-08-876- Sequence 10, Applicati	4.81e-07
8	196	11.1	27	1	US-08-165- Sequence 10, Applicati	4.81e-07
9	110	6.2	27	1	US-08-876- Sequence 11, Applicati	1.52e+00
10	110	6.2	27	2	US-08-876- Sequence 11, Applicati	1.52e+00
11	109	6.2	305	2	US-08-946- Sequence 1, Applicatio	1.78e+00
12	99	5.6	174	1	US-08-261- Sequence 2, Applicatio	8.83e+00
13	99	5.6	174	2	US-08-261- Sequence 2, Applicatio	8.83e+00
14	99	5.6	174	3	US-08-719- Sequence 2, Applicatio	8.83e+00
15	96	5.4	25	2	US-08-220- Sequence 3, Applicatio	1.41e+01
16	96	5.4	25	2	US-08-696- Sequence 3, Applicatio	1.41e+01
17	96	5.4	28	1	US-08-220- Sequence 7, Applicatio	1.41e+01
18	96	5.4	28	2	US-08-696- Sequence 7, Applicatio	1.41e+01
19	94	5.3	971	2	US-08-724- Sequence 22, Applicati	1.93e+01
20	91	5.2	299	2	US-09-047- Sequence 24, Applicati	3.07e+01
21	90	5.1	23	1	US-08-220- Sequence 5, Applicatio	3.58e+01
22	90	5.1	23	2	US-08-696- Sequence 5, Applicatio	3.58e+01
23	90	5.1	451	1	US-08-417- Sequence 12, Applicati	3.58e+01

ID	US-08-446-918A-2	STANDARD:	PRT:	255 AA.		
24	90	5.1	2296	2	US-08-286- Sequence 27, Applicati	3.58e+01
25	88	5.0	364	1	US-08-423- Sequence 6, Applicatio	4.85e+01
26	89	5.0	492	1	US-08-417- Sequence 14, Applicati	4.17e+01
27	88	5.0	1296	1	US-08-480- Sequence 28, Applicati	4.85e+01
28	88	5.0	1296	2	US-08-405- Sequence 28, Applicati	4.85e+01
29	87	4.9	27	2	US-08-876- Sequence 13, Applicati	5.65e+01
30	87	4.9	27	1	US-08-165- Sequence 13, Applicati	5.65e+01
31	87	4.9	308	2	US-09-047- Sequence 23, Applicatio	5.65e+01
32	87	4.9	314	1	US-08-040- Sequence 2, Applicatio	5.65e+01
33	87	4.9	421	2	US-08-807- Sequence 16, Applicati	5.65e+01
34	87	4.9	462	1	US-08-417- Sequence 3, Applicatio	5.65e+01
35	86	4.9	516	2	US-09-019- Sequence 11, Applicati	5.65e+01
36	87	4.9	593	3	PCT-US93-0 Sequence 3, Applicatio	5.65e+01
37	87	4.9	755	3	PCT-US93-0 Sequence 3, Applicatio	5.65e+01
38	87	4.9	759	3	PCT-US93-0 Sequence 2, Applicatio	5.65e+01
39	86	4.9	759	2	US-08-450- Sequence 4, Applicatio	5.65e+01
40	87	4.9	766	1	US-08-619- Sequence 3, Applicatio	5.65e+01
41	87	4.9	766	2	US-08-940- Sequence 3, Applicatio	5.65e+01
42	87	4.9	766	1	US-08-230- Sequence 3, Applicatio	5.65e+01
43	86	4.9	1003	1	US-07-991- Sequence 6, Applicatio	6.57e+01
44	86	4.9	1003	2	US-08-544- Sequence 6, Applicatio	6.57e+01
45	86	4.9	1003	1	US-08-107- Sequence 6, Applicatio	6.57e+01

ALIGNMENTS

RESULT 1
ID US-08-446-918A-2 STANDARD: PRT: 255 AA.
AC xxxxxx
DT
XX
DE
XX
Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 255 AA: 30159 MW: 364503 CN:

Query Match	99.8%	Score 1760;	DB 1;	length 255;
Best Local Similarity	99.6%	Pred. No. 1,55e-143;		
Matches 238;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Db	17 ESQDPKPEDELHKSSKFTGLMENKKVLYDDNHSAINVKSIDQELFYDLYSIKDTKLG	76		
Qy	1 ESQDPKPEDELHKSSKFTGLMENKKVLYDDNHSAINVKSIDQELFYDLYSIKDTKLG	60		
Db	77 YDNVREKKNLDLADKYDKYVDFGANYYYQCFESKNTDINSHQDPDKRTCMYGGVTE	136		
Qy	61 YDNVREKKNLDLADKYDKYVDFGANYYYQCFESKNTDINSHEDKRTCMYGGVTE	120		
Db	137 HNGNOLDKYSITVRFVEDEKNNLSFDVQYTKKKVTAQELDYLTRHYLYNKKKLYEFNNS	196		
Qy	121 HNGNOLDKYSITVRFVEDEKNNLSFDVQYTKKKVTAQELDYLTRHYLYNKKKLYEFNNS	180		
Db	197 PYENGUYKEIFENENSPWDDMPAPGDKRFDQSKYLYAMYNNDKNMVSQDKYKIEVYLTTRKK	255		
Qy	181 PYENGUYKEIFENENSPWDDMPAPGDKRFDQSKYLYAMYNNDKNMVSQDKYKIEVYLTTRKK	239		

RESULT	2			
ID	US-08-580-806-2	STANDARD:	PRT:	255 AA.
XX	xxxxxx			
AC				
DT				
XX				
DE	Sequence 2, Application US/08580806			
CC	Sequence 2, Application US/08580806			
CC	Patent No. 5935568			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Dow, Steve W.			
CC	APPLICANT: Elmslie, Robyn E.			
CC	APPLICANT: Potter, Terence A.			
CC	TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION			
CC	NUMBER OF SEQUENCES: 13			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: Sheridan Ross & McIntosh			
CC	STREET: 1700 Lincoln Street, Suite 3500			
CC	City: Denver			
CC	STATE: Colorado			
CC	COUNTRY: U.S.A.			
CC	Zip: 80203			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/580,806			
CC	FILING DATE:			
CC	CLASSIFICATION: 424			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Connell, Gary J.			
CC	REGISTRATION NUMBER: 32,020			
CC	REFERENCE/DOCKET NUMBER: 2879-29-C1			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (303) 863-9700			
CC	TELEFAX: (303) 863-0223			
CC	INFORMATION FOR SEQ ID NO: 2:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 255 amino acids			
CC	Type: amino acid			
CC	TOPOLOGY: linear			
CC	MOLECULE TYPE: protein			
CC	SEQUENCE 255 AA; 30159 MW; 364503 CN;			
SO				
Query Match	99.8%; Score 1760; DB 2; Length 255;			
Best Local Similarity	99.6%; Pred. No.1,55e-143;			
Matches 236; Conservative	1; Mismatches 0; Indels 0; Gaps 0;			

Db	17	ESODPRDELHSSKFFGLMENNKYLYDDNHSAINVKSIDOLFEDLITSJKDRKLN	76
Qy	1	ESQDPKPELDHAKSSKFFGLMENNKYLYDDNHSAINVKSIDOLFEDLITSJKDRKLN	60
Db	77	YDNRVVEKKNLDLADKPKDKYVDVFGANYYYOCYFSKRTNDINSHQTDKRRKTCMGVTE	136
Qy	61	YDNRVVEKKNLDLADKPKDKYVDVFGANYYYOCYFSKRTNDINSHETDKRRKTCMGVTE	120
Db	137	HNGNOLDKRYRSITRYRVFEDGKNLLSPVOYNNKKKVTQOEIDLYLTRHLYVNNKKLYEPNNS	136
Qy	121	HNGNOLDKRYRSITRYRVFEDGKNLLSPVOYNNKKKVTQOEIDLYLTRHLYVNNKKLYEPNNS	180
Db	197	PYENGYYIKFIEINENSFWDDMAPAGDFKFDOSKYLTAMYNDNKKMYSKDYKLEVLTTKKK	255
Qy	181	PYENGYYIKFIEINENSFWDDMAPAGDFKFDOSKYLTAMYNDNKKMYSKDYKLEVLTTKKK	239

[illegible]

[illegible]

QY	128	KYRSTTVAVEEDGK-NLISFP-VQTNKKKTAQELDYLTRHYLVKNNKLEFPN--NSPEY 1033
DB	181	RGLIHFHSTEPSVNYDLFGAGG-YSNT-DLRIYRDNKKTINSEMHIDIYLYT 232
QY	184	TGYINF-IENENSFMYIDMMPAPGDKFQDSKYLMMYNDRKNWDSKDVIEYLYTT 236
RESULT	5	
ID	US-08-876-781-9	STANDARD; PRT; 27 AA.
XX	xxxxxx	
DT		
XX		
DE	Sequence 9, Application US/08876781	
XX		
CC	Sequence 9, Application US/08876781	
CC	Patent No. 5872233	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Cole, Barry C.	
CC	APPLICANT: Atkin, Curtis L.	
CC	APPLICANT: Pole, Ann	
CC	APPLICANT: Oliphant, Arnold	
CC	TITLE OF INVENTION: Mycoplasma Arthritis T-Cell	
CC	TITLE OF INVENTION: M10gen	
CC	NUMBER OF SEQUENCES: 26	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Thorpe, No. 5872233th & Western	
CC	STREET: 9035 South 700 East, Suite 200	
CC	CITY: Sandy	
CC	STATE: Utah	
CC	COUNTRY: USA	
CC	ZIP: 84070	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Diskette, 3.5 inch, 720 kb storage	
CC	COMPUTER: AST Advantage NB-SX20	
CC	OPERATING SYSTEM: DOS 5.00	
CC	SOFTWARE: Word Perfect 5.1	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: US/08/876,781	
CC	FILING DATE:	
CC	CLASSIFICATION: 424	
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	
CC	FILING DATE:	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: M. Wayne Western	
CC	REGISTRATION NUMBER: 22,788	
CC	REFERENCE/DOCKET NUMBER: T676	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (801)566-6633	
CC	TELEFAX: (801)566-0750	
CC	INFORMATION FOR SEQ ID NO: 9:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 27 amino acids	
CC	TYPE: amino acid	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: peptide	
CC	FRAGMENT TYPE: Internal fragment	
CC	ORIGINAL SOURCE:	
CC	ORGANISM: Staphylococcus aureus	
CC	STRAIN: S6	
CC	CELL TYPE: unicellular organism	
CC	FEATURE:	
CC	NAME/KEY: staphylococcal enterotoxin B amino acid	
CC	NAME/KEY: sequence having sequence similarity to	
CC	NAME/KEY: MAM.	
CC	LOCATION: residues 39 to 65	
CC	IDENTIFICATION METHOD: computer searching for	
CC	IDENTIFICATION METHOD: sequence similarities.	
CC	PUBLICATION INFORMATION:	
CC	AUTHORS: Jones, C.L.	

CC AUTHORS: Khan, S.A.
CC TITLE: Nucleotide Sequence of the Enterotoxin B
CC Patent No. 5872233
CC TITLE: Gene from Staphylococcus aureus
CC JOURNAL: J. Bacteriol.
CC VOLUME: 166
CC ISSUE: 1
CC PAGES: 29-33
CC DATE: APR-1986
SQ SEQUENCE 27 AA; 3270 MW; 3891 CN;

Query Match 11.4%; Score 201; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.93e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 KSIDQFLYFDLIYSIKPTKLGNYDNVR 27
QY 39 KSIDQFLYFDLIYSIKPTKLGNYDNVR 65

RESULT 6 STANDARD: PRT: 27 AA.
ID US-08-165-038-9
AC xxxxxx
DT
XX
XX
Sequence 9, Application US/08165038
CC Patent No. 5639869
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5639869th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
CC COMPUTER: AST Advantage NB-SX20
CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165,038
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788
CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 9:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORIGINAL SOURCE:

CC ORGANISM: Staphylococcus aureus
CC STRAIN: S6
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin B amino acid
CC NAME/KEY: sequence having sequence similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 39 to 65
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Jones, C.L.
CC AUTHORS: Khan, S.A.
CC TITLE: Nucleotide Sequence of the Enterotoxin B
CC Patent No. 5639869
CC TITLE: Gene from Staphylococcus aureus
CC JOURNAL: J. Bacteriol.
CC VOLUME: 166
CC ISSUE: 1
CC PAGES: 29-33
CC DATE: APR-1986
SQ SEQUENCE 27 AA; 3270 MW; 3891 CN;

Query Match 11.4%; Score 201; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.93e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 KSIDQFLYFDLIYSIKPTKLGNYDNVR 27
QY 39 KSIDQFLYFDLIYSIKPTKLGNYDNVR 65

RESULT 7 STANDARD: PRT: 27 AA.
ID US-08-876-781-10
AC xxxxxx
DT
XX
XX
Sequence 10, Application US/08876781
CC Patent No. 5872233
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5872233th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
CC COMPUTER: AST Advantage NB-SX20
CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/876,781
CC FILING DATE:
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788

CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORIGINAL SOURCE:
CC ORGANISM: Staphylococcus aureus
CC STRAIN: 56
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin B amino acid
CC NAME/KEY: sequence having sequence similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 56 to 82
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Jones, C.L.
CC AUTHORS: Khan, S.A.
CC TITLE: Nucleotide Sequence of the Enterotoxin B
CC Patent No. 5872233
CC TITLE: Gene from Staphylococcus aureus
CC JOURNAL: J. Bacteriol.
CC VOLUME: 166
CC ISSUE: 1
CC PAGES: 29-33
CC DATE: APR-1986
CC SEQUENCE 27 AA; 3265 MM; 4119 CN;
SQ
Query Match 11.1%; Score 196; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.81e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TKLGNDVNVREFFKNKDLADKKYKRV 27
OY 56 TKLGNDVNVREFFKNKDLADKKYKRV 82
RESULT 8
ID US-08-165-038-10 STANDARD; PRT; 27 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 10, Application US/08165038
XX
CC Sequence 10, Application US/08165038
CC Patent No. 5639869
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC TITLE OF INVENTION: Mitogen
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: Thorpe, No. 5639869th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
CC COMPUTER: ASR Advantage NB-SX20

CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165,038
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788
CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORIGINAL SOURCE:
CC ORGANISM: Staphylococcus aureus
CC STRAIN: 56
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin B amino acid
CC NAME/KEY: sequence having sequence similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 56 to 82
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Jones, C.L.
CC AUTHORS: Khan, S.A.
CC TITLE: Nucleotide Sequence of the Enterotoxin B
CC Patent No. 5639869
CC TITLE: Gene from Staphylococcus aureus
CC JOURNAL: J. Bacteriol.
CC VOLUME: 166
CC ISSUE: 1
CC PAGES: 29-33
CC DATE: APR-1986
CC SEQUENCE 27 AA; 3265 MM; 4119 CN;
SQ
Query Match 11.1%; Score 196; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.81e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TKLGNDVNVREFFKNKDLADKKYKRV 27
OY 56 TKLGNDVNVREFFKNKDLADKKYKRV 82
RESULT 9
ID US-08-165-038-11 STANDARD; PRT; 27 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 11, Application US/08165038
XX
CC Sequence 11, Application US/08165038
CC Patent No. 5639869
CC GENERAL INFORMATION:
CC APPLICANT: Cole, Barry C.
CC APPLICANT: Atkin, Curtis L.
CC APPLICANT: Pole, Ann
CC APPLICANT: Oliphant, Arnold
CC TITLE OF INVENTION: Mycoplasma Arthritis T-Cell

```

CC TITLE OF INVENTION: Mitogen
CC NUMBER OF SEQUENCES: 26
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Thorpe, No. 5639869th & Western
CC STREET: 9035 South 700 East, Suite 200
CC CITY: Sandy
CC STATE: Utah
CC COUNTRY: USA
CC ZIP: 84070
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.5 inch, 720 kb storage
CC COMPUTER: AST Advantage NB-SX20
CC OPERATING SYSTEM: DOS 5.00
CC SOFTWARE: Word Perfect 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/165, 038
CC FILING DATE:
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: M. Wayne Western
CC REGISTRATION NUMBER: 22,788
CC REFERENCE/DOCKET NUMBER: T676
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (801)566-6633
CC TELEFAX: (801)566-0750
CC INFORMATION FOR SEO ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 27 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC FRAGMENT TYPE: internal fragment
CC ORIGINAL SOURCE:
CC ORGANISM: Staphylococcus aureus
CC CELL TYPE: unicellular organism
CC FEATURE:
CC NAME/KEY: staphylococcal enterotoxin C1 amino acid
CC NAME/KEY: sequence having sequence similarity to
CC NAME/KEY: MAM.
CC LOCATION: residues 30 to 56
CC IDENTIFICATION METHOD: computer searching for
CC IDENTIFICATION METHOD: sequence similarities.
CC PUBLICATION INFORMATION:
CC AUTHORS: Bonach, G.A.
CC AUTHORS: Schleifert, P.M.
CC TITLE: Nucleotide sequence of the staphylococcal
CC TITLE: enterotoxin C1 gene and relatedness to
CC TITLE: other pyrogenic exotoxins
CC JOURNAL: Mol. Gen. Genet.
CC VOLUME: 209
CC PAGES: 15-20
CC DATE: 1987
SQ SEQUENCE 27 AA: 3107 MW: 4022 CN:

Query Match 6.2%; Score 110; DB 1; Length 27;
Best Local Similarity 61.5%; Pred. No. 1.52e+00;
Matches 16; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 1 DHVSAATKRVKSVDFKLAHDLIYNISD 26
|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 30 DNHVSAINWKSIDDFLFDLITISIKD 55

RESULT 10 STANDARD; PRT; 27 AA.
XX US-08-876-781-11
AC xxxxxx
XX
XX
XX

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DE      Sequence 11, Application US/08876781
XX
CC      Sequence 11, Application US/08876781
CC      Patent No. 5872233
CC      GENERAL INFORMATION:
CC      APPLICANT: Cole, Barry C.
CC      APPLICANT: Atkin, Curtis L.
CC      APPLICANT: Pole, Ann
CC      APPLICANT: Oliphant, Arnold
CC      TITLE OF INVENTION: Mycoplasma Arthritis T-Cell
CC      TITLE OF INVENTION: Mitogen
CC      NUMBER OF SEQUENCES: 26
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Thorpe, No. 5872233th & Western
CC      STREET: 9035 South 700 East, Suite 200
CC      CITY: Sandy
CC      STATE: Utah
CC      COUNTRY: USA
CC      ZIP: 84070
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Diskette, 3.5 Inch, 720 Kb storage
CC      COMPUTER: ASP Advantage NB-SX20
CC      OPERATING SYSTEM: DOS 5.00
CC      SOFTWARE: Word Perfect 5.1
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/876,781
CC      FILING DATE:
CC      CLASSIFICATION: 424
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER:
CC      FILING DATE:
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: M. Wayne Western
CC      REGISTRATION NUMBER: 22,788
CC      REFERENCE/DOCKET NUMBER: T676
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (801)566-6633
CC      TELEFAX: (801)566-0750
CC      INFORMATION FOR SEQ ID NO: 11:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 27 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: peptide
CC      FRAGMENT TYPE: Internal fragment
CC      ORIGINAL SOURCE:
CC      ORGANISM: Staphylococcus aureus
CC      CELL TYPE: unicellular organism
CC      FEATURE:
CC      NAME/KEY: staphylococcal enterotoxin CI amino acid
CC      NAME/KEY: sequence having sequence similarity to
CC      NAME/KEY: MAM.
CC      LOCATION: residues 30 to 56
CC      IDENTIFICATION METHOD: computer searching for
CC      IDENTIFICATION METHOD: sequence similarities.
CC      PUBLICATION INFORMATION:
CC      AUTHORS: Bohach, G.A.
CC      AUTHORS: Schlevert, P.M.
CC      TITLE: Nucleotide sequence of the staphylococcal
CC      TITLE: enterotoxin CI gene and relatedness to
CC      TITLE: other pyrogenic exotoxins
CC      JOURNAL: Mol. Gen. Genet.
CC      VOLUME: 209
CC      PAGES: 15-20
CC      DATE: 1987
CC      SEQUENCE 27 AA; 3107 MW; 4022 CN;
SQ
Query Match          6.2%   Score 110; DB 2; Length 27;
Best Local Similarity 61.5%; Pred. No. 1.5e+00;
Matches    16; Conservative    4; Mismatches    6; Indels    0; Gaps    0;
db       1 DHVYATKRVKSVDKFLAHDLYINISD 26
1: ||| :|||: | |||:
```

[illegible]

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XX      xxxxxx  
AC  
DT  
Sequence 2, Application US/08261825  
DE  
Sequence 2, Application US/08261825  
CC Patent No. 5558993  
CC GENERAL INFORMATION:  
CC APPLICANT: Champion, Cheryl I.  
CC APPLICANT: Lovett, Michael A.  
CC APPLICANT: Haake, David A.  
CC APPLICANT: Miller, James N.  
CC APPLICANT: Blanco, David R.  
CC TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE  
CC TITLE OF INVENTION: PROTEIN  
CC NUMBER OF SEQUENCES: 8  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Spensley Horn Jubas & Lubitz  
CC STREET: 1880 Century Park East, Suite 500  
CC CITY: Los Angeles  
CC STATE: California  
CC COUNTRY: USA  
CC ZIP: 90067  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patentin Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/261,825  
CC FILING DATE: 17-JUN-1994  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: TUMARKIN, LISA A.  
CC REGISTRATION NUMBER: P-38,347  
CC REFERENCE/DOCKET NUMBER: PD3516  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (619) 455-5100  
CC TELEFAX: (619) 455-5110  
CC INFORMATION FOR SEQ ID NO: 2:  
CC     SEQUENCE CHARACTERISTICS:  
CC         LENGTH: 174 amino acids  
CC             type: amino acid  
CC             TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 174 AA; 20290 MW; 153533 CN;  
SQ  
  
Query Match          5.6%; Score 99; DB 1; Length 174;  
Best Local Similarity 29.2%; Pred.No. 8.83e+00;  
Matches    26; Conservative   25; Mismatches 32; Indels 6; Gaps 6;  
  
Db       65 AKAPRISRLKRTGKEN-STVLALDVYGYTKSKITTPDLSFIIMINSLIKGPNSIF 123  
        6 .KKPEPLHKSSTFTGITLMMKVLYDD-MNVSAIINVXSIDQFL-YFDL-IYS-INKDKLGNY 61  
DB       124 DYILQLDSKDIDVAEKYGAKARENPEEY 152  
        |::: :|::|| :: || ::  
DY       62 DN-VAVEFKNKDLADKYIKDIYDFVGANY 89  
  
RESULT  13  
ID      PCt-US95 -07748A -2           STANDARD;            PRt;    174 AA.  
XX      xxxxxxxx  
DT  
Sequence 2, Application PC/TUS9507748A  
XX  
Sequence 2, Application PC/TUS9507748A  
CC GENERAL INFORMATION:
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[illegible]

CC	COUNTRY: USA
CC	ZIP: 90067
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: Patentin Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: US/08/719,124
CC	FILING DATE: 24-SEP-1996
CC	CLASSIFICATION: 530
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: 08/261,825
CC	FILING DATE: 17-JUN-1994
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: TUMARKIN, LISA A.
CC	REGISTRATION NUMBER: P-38,347
CC	REFERENCE/DOCKET NUMBER: PD3516
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (619) 455-5100
CC	TELEFAX: (619) 455-5110
CC	INFORMATION FOR SEQ ID NO: 2:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 174 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
CC	SEQUENCE 174 AA; 20290 MM; 153533 CN;
CC	Query Match 5.6%; Score 99; DB 2; Length 174;
CC	Best Local Similarity 29.2%; Pred. No. 8.83e+00;
CC	Matches 26; Conservative 25; Mismatches 32; Indels 6; Gaps 6;
Db	65 AKAEIRNSLRKIKIKEN-SVLDALDVGFIRKSRITFDLSPIIMINSLIKGYPSNISF 123
QY	6 PKPELHKSSFTGLMEMKVLDD-NHVSAINKSLDQFL-YRDL-IYS-IKOTKIGN 61
Db	124 DYLIQLDSDKIDYAEKIGERKARENEESY 152
QY	62 DN-VRVEFKNKDLADKYKDYVDEGANY 89
RESULT 15	
ID	US-08-220-378-3 STANDARD; PRT; 25 AA.
XX	xxxxxx
AC	
DT	
DE	Sequence 3, Application US/08220378
XX	
CC	Sequence 3, Application US/08220378
CC	Patent No. 5545716
CC	GENERAL INFORMATION:
CC	APPLICANT: Johnson, Howard M.
CC	APPLICANT: Pontzer, Carol H.
CC	APPLICANT: Griggs, Nathan D.
CC	TITLE OF INVENTION: Superantigen Agonist and Antagonist
CC	TITLE OF INVENTION: Peptides
CC	NUMBER OF SEQUENCES: 10
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Saliwanichik & Saliwanichik
CC	STREET: 2421 N.W. 41st Street, Suite A-1
CC	CITY: Gainesville
CC	STATE: FL
CC	COUNTRY: USA
CC	ZIP: 32606
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: Patentin Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:

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(TM)

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.....NKWDSKDKIEVYLTTKK 239

Chapter 11

88963 seqs, 23686106 residues

isting first 45 summaries

1: geneseqp

mean 32.417; Variance 153.333; scale 0.211

and is derived by analysis of the total score distribution.

SUMMARIES

Staphylococcus enterot 8.39e-54

45	726	41.2	190	1	R42011	Staphylococcus enterot	4.92e-52
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ALIGNMENTS

Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query match 100.0%; Score 1763; DB 1; Length 239;

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Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLG 60

QY 1 ESQPPKPEDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLG 60

Db 61 YDNVRVEFKNKDLADKYYKDKYVDVEFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE 120

QY 61 YDNVRVEEKNKDLADKYYKDKYVDVEFGANYYYQCYFSKKTNDINSHETDKRKTCMYGGVTE 120

DB 121 HNGNOLDKRSITVRFEDEGKNILSFVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 OY 121 HNGNOLDKRSITVRFEDEGKNILSFVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 DB 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLMYNDNKWVDSKDVKIEVYLTTRKK 239
 OY 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLMYNDNKWVDSKDVKIEVYLTTRKK 239

RESULT 2

ID M06737 standard; Protein: 255 AA.
 AC M06737;
 DT 08-MAR-1997 (first entry)
 DE Staphylococcus enterotoxin B.
 KM Enterotoxin B: superantigen; antigen; cytokine; chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer;
 OS vaccine; adjuvant.
 FT Staphylococcus sp.
 FH Key Location/Qualifiers
 FT peptide 1..15
 FT /label= Sig-peptide
 PN M09636366-A1.
 PD 21-NOV-1996.
 PR 20-MAY-1996; U07432.
 PR 18-MAY-1995; US-446918.
 PR 29-DEC-1995; US-580806.
 PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY MED.
 PI Dow SW, Elmslie RE, Potter RA;
 DR N-PSDB; T45697.
 DT WPI: 97-01187/01.
 PT Recombinant molecule encoding super:antigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer
 PS Example 1: Page 96-97; 131pp. English.
 CC A cDNA clone (T45698) codes for staphylococcal enterotoxin B
 CC (M06737) superantigen. Nucleic acids encoding superantigens (see
 CC also M06738-39), esp. truncated forms of the superantigen lacking
 CC the leader peptide, can be utilised in the gene therapy of cancer,
 CC infectious diseases and immunological disorders. The nucleic acid,
 CC optionally in combination with cytokine or chemokine nucleic acids,
 CC is delivered to an animal using e.g. liposomes. It acts by
 CC controlling the activity of effector cells, such as T-cells,
 CC macrophages, monocytes and/or natural killer cells. Localised
 CC prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal.
 SQ Sequence 255 AA.

Query Match 99.8%; Score 1760; DB 1; Length 255;
 Best Local Similarity 99.6%; Pred. No. 9.88e-145;
 Matches 238; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 17 ESQPDKPELHKSSKFTGLMENMKVLYDDNHVSAINVSIDQFLFYDLIYSIKDTKLG 76
 OY 1 ESQPDKPELHKSSKFTGLMENMKVLYDDNHVSAINVSIDQFLFYDLIYSIKDTKLG 60
 DB 77 YDNVREFFKNKDLADYKXKYVDVFGANYCYCFSKKTNDINSHTDRKCTMGVTE 136
 OY 61 YDNVREFFKNKDLADYKXKYVDVFGANYCYCFSKKTNDINSHTDRKCTMGVTE 120
 DB 137 HNGNOLDKRSITVRFEDEGKNILSFVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 196
 OY 121 HNGNOLDKRSITVRFEDEGKNILSFVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 DB 197 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLMYNDNKWVDSKDVKIEVYLTTRKK 255
 OY 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLMYNDNKWVDSKDVKIEVYLTTRKK 239

RESULT 3
 ID R13206 standard; Protein: 239 AA;
 AC R13206;
 DT 15-OCT-1991 (first entry)
 DE Staphylococcal enterotoxin B.

KW SEB; cancer treatment; pyrogen; tumouricide.
 OS Staphylococcus aureus.
 PN M09110680-A.
 PD 25-JUL-1991.
 PR 17-JAN-1991; U00342.
 PR 17-JAN-1990; US-466577.
 PA (TERM/) TERMAN D S.
 PI Terman DS;
 DR WPI: 91-237984/32.
 PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity
 PT as Staphylococcal protein A without potential toxic reactions
 PS Disclosure; Fig 1; 74pp. English.
 CC SEB was isolated and purified from S. aureus. It can be used for
 CC treating cancer, activating cytokine mediators and procoagulant
 CC systems, augmenting natural killer cell cytotoxicity, etc. The
 CC enterotoxin can be administered intravenously, optionally with
 CC ibuprofen to attenuate toxic reaction to SEB. Synthetic
 CC polypeptides having structural homology to Staphylococcal exotoxins
 CC are claimed, provided the homology includes statistically
 CC significant sequence homology, alignment of Cysteine residues and
 CC similar hydropathy profiles.
 CC See R13203-R13211.
 SQ Sequence 239 AA.

Query Match 97.8%; Score 1725; DB 1; Length 239;
 Best Local Similarity 97.9%; Pred. No. 1.44e-141;
 Matches 234; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 1 ESQPDKPELHKSSKFTGLMENMKVLYDDNHVSAINVSIDQFLFYDLIYSIKDTKLG 60
 OY 1 ESQPDKPELHKSSKFTGLMENMKVLYDDNHVSAINVSIDQFLFYDLIYSIKDTKLG 60
 DB 61 YDNVREFFKNKDLADYKXKYVDVFGANYCYCFSKKTNDINSHTDRKCTMGVTE 120
 OY 61 YDNVREFFKNKDLADYKXKYVDVFGANYCYCFSKKTNDINSHTDRKCTMGVTE 120
 DB 121 HNGNOLDKRSITVRFEDEGKNILSFVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 OY 121 HNGNOLDKRSITVRFEDEGKNILSFVOTNKKVTAQELDYLTRHYLVKNNKLYEFNNS 180
 DB 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLMYNDNKWVDSKDVKIEVYLTTRKK 239
 OY 181 PYETGYIKFIENENSWFYDMMPAPGDKFQOSKYLMYNDNKWVDSKDVKIEVYLTTRKK 239

RESULT 4

ID R45014 standard; Protein: 239 AA.
 AC R45014;
 DT 08-JUN-1994 (first entry)
 DE Staphylococcal enterotoxin SEB.
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 OS autoimmune disease; toxicity; Protein A; pertussis system.
 PN M09324136-A.
 PD 09-DEC-1993.
 PR 01-JUN-1993; U05213.
 PR 01-JUN-1992; US-891718.
 PA (STON/) STONE J L.
 PA (TERM/) TERMAN D S.
 PI Stone JL, Terman DS;
 DR WPI: 93-405418/50.
 PT use of staphylococcal enterotoxin(s) and homologues - for
 PT treating cancer in a patient or for the treatment of auto-immune
 PT diseases
 PS Disclosure; Fig 1; 90pp. English.
 CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer
 CC in a patient. These SEs, and homologues of them, can be used as
 CC tumouricidal agents for treating cancers and autoimmune disease.
 CC They exhibit tumouricidal activity and toxicity identical to that
 CC observed for the protein A pertussis system. They may be administered
 CC by i.v. injection.

SO Sequence 239 AA;

Query Match 97.8%; Score 1725; DB 1; Length 239;
Best Local Similarity 97.8%; Pred. No. 1,44e-141;
Matches 234; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 ESQDPKPEDELHKSSKFTGLMNMKVLYDDNHVSAINVKSIDOFLYFDLISIKDKLGN 60
QY 1 ESQDPKPEDELHKSSKFTGLMNMKVLYDDNHVSAINVKSIDOFLYFDLISIKDKLGN 60
Db 61 YDNVVEREKNKDLADKYKDYVDGANYYYQCYFSKRTNDINSHQTDKRTKMGVYTE 120
QY 61 YDNVVEREKNKDLADKYKDYVDGANYYYQCYFSKRTNDINSHQTDKRTKMGVYTE 120
Db 121 HNGNOLDKRYRSLITVAFEDGKNLSFDVQTNKKVTAQELDYLTRHLYLVKKNKLYEFNNS 180
QY 121 HNGNOLDKRYRSLITVAFEDGKNLSFDVQTNKKVTAQELDYLTRHLYLVKKNKLYEFNNS 180
Db 181 PYETGYIKFIENENSFWDLPAPGDKFDQSKYLLMNYNDKNKVDSDVKIEVYLTKKK 239
QY 181 PYETGYIKFIENENSFWDLPAPGDKFDQSKYLLMNYNDKNKVDSDVKIEVYLTKKK 239

RESULT 5
ID R45015 standard; protein; 239 AA.
AC R45015;
DT 08-JUN-1994 (first entry)
DE Staphylococcal enterotoxin SEc1.
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
OS Staphylococcus aureus.
PN MO9324136-A.
PD 09-DEC-1993.
PE 01-JUN-1993; U05213.
PF 01-JUN-1992; US-891718.
PA (STON/) STONE J L.
PA (TERM/) TERMAN D S.
PI Stone J L, Terman D S;
DR WPI; 93-405418/50.
PT Use of staphylococcal enterotoxin(s) and homologues - for
treating cancer in a patient or for the treatment of auto-immune
PT diseases
PS Disclosure; Fig 1; 90pp; English.
CC The sequences given in R45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer
CC in a patient. These SEs, and homologues of them, can be used as
CC tumouricidal agents for treating cancers and autoimmune disease.
CC They exhibit tumouricidal activity and toxicity identical to that
CC observed for the protein A perfusion system. They may be administered
CC by i.v. injection.
CC Sequence 239 AA;

Query Match 66.7%; Score 1176; DB 1; Length 239;
Best Local Similarity 66.4%; Pred. No. 3.93e-92;
Matches 160; Conservative 41; Mismatches 34; Indels 6; Gaps 6;

Db 1 ESQDPKPEDELHKSSKFTGLMNMKVLYDDHYVSAFKVSVDKFLAHLIYNISDKLKN 60
QY 1 ESQDPKPEDELHKSSKFTGLMNMKVLYDDNHVSAINVKSIDOFLYFDLISIKDKLGN 60
Db 61 YDKVTELLNEGLAKKRYKDEVDVYGSNYYVNCYFSSK-DNV-GKVTG-G-KTCMGGITK 117
QY 61 YDNVVEREKNKDLADKYKDYVDGANYYYQCYFSKRTNDINSHQTDKRTKMGVYTE 120
Db 118 HGNFNDGNLQNLVIRYVENKRNITISFEVOTDKKSVTAQELDIARPNFLIKKNLYEFN 177
QY 121 HNGNOLDK-Y-RSLTVRFEDEKKNLSFDVQTNKKVTAQELDYLTRHLYLVKKNKLYEFN 178
Db 178 SSPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLLMNYNDKNKTVDSKSVKIEVHLFTK 237
QY 179 NSPYETGYIKFIENE-NSFWYDMMPAPGDKFDQSKYLLMNYNDKNKVDSDVKIEVYLTKK 237
Db 238 N 238

QY 238 K 238

RESULT 6
ID R13207 standard; protein; 239 AA.
AC R13207;
DT 15-OCT-1991 (first entry)
DE Staphylococcal enterotoxin C1.
KW SEc1; cancer treatment; pyrogen; tumouricide.
OS Staphylococcus aureus.
PN MO9110680-A.
PD 25-JUL-1991.
PE 17-JAN-1991; U00342.
PF 17-JAN-1990; US-465577.
PA (TERM/) TERMAN D S.
PI Terman D S;
DR WPI; 91-237984/32.
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity
PT as Staphylococcal protein A without potential toxic reactions
PS Disclosure; Fig 1; 74pp; English.
CC SEc1 was isolated and purified from S.aureus. It can be used for
CC treating cancer, activating cytokine mediators and procoagulant
CC systems, augmenting natural killer cell cytotoxicity, etc. The
CC enterotoxin can be administered intravenously, optionally with
CC lipoprotein to attenuate toxic reaction to SEc1. Synthetic
CC polypeptides having structural homology to staphylococcal exotoxins
CC are claimed, provided the homology includes statistically
CC significant sequence homology, alignment of cysteine residues and
CC similar hydropathy profiles.
CC See R13203-R13211.
CC Sequence 239 AA;

Query Match 66.7%; Score 1176; DB 1; Length 239;
Best Local Similarity 66.4%; Pred. No. 3.93e-92;
Matches 160; Conservative 41; Mismatches 34; Indels 6; Gaps 6;

Db 1 ESQDPKPEDELHKSSKFTGLMNMKVLYDDHYVSAFKVSVDKFLAHLIYNISDKLKN 60
QY 1 ESQDPKPEDELHKSSKFTGLMNMKVLYDDNHVSAINVKSIDOFLYFDLISIKDKLGN 60
Db 61 YDKVTELLNEGLAKKRYKDEVDVYGSNYYVNCYFSSK-DNV-GKVTG-G-KTCMGGITK 117
QY 61 YDNVVEREKNKDLADKYKDYVDGANYYYQCYFSKRTNDINSHQTDKRTKMGVYTE 120
Db 118 HGNFNDGNLQNLVIRYVENKRNITISFEVOTDKKSVTAQELDIARPNFLIKKNLYEFN 177
QY 121 HNGNOLDK-Y-RSLTVRFEDEKKNLSFDVQTNKKVTAQELDYLTRHLYLVKKNKLYEFN 178
Db 178 SSPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLLMNYNDKNKTVDSKSVKIEVHLFTK 237
QY 179 NSPYETGYIKFIENE-NSFWYDMMPAPGDKFDQSKYLLMNYNDKNKVDSDVKIEVYLTKK 237
Db 238 N 238

QY 238 K 238

RESULT 7
ID R45016 standard; protein; 238 AA.
AC R45016;
DT 08-JUN-1994 (first entry)
DE Staphylococcal enterotoxin SEc3.
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
OS Staphylococcus aureus.
PN MO9324136-A.
PD 09-DEC-1993.
PE 01-JUN-1993; U05213.
PF 01-JUN-1992; US-891718.
PA (STON/) STONE J L.
PA (TERM/) TERMAN D S.

DE Staphylococcus enterotoxin B mutant BR-21.
KM Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
KM random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
KM autoimmune disease.
OS Staphylococcus aureus.
FH Key
FT Location/Qualifiers
FT 97..157
FT /note-"Region undisclosed in the specification"
FT 162..186
FT /note-"Region undisclosed in the specification"
FT region
FT WO9314634-A.
PD 05-AUG-1993.
PD 28-JAN-1993. U00839.
PR 28-JAN-1992; US-827540.
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
PI Kappeler JW, Marrack P;
DR WPI; 93-320314/40.
PT Preventing or treating toxic effects of super antigens - by admin. of
PT new modified or mutated super antigen which induces antibodies but
PT not T-cell activation
PS Disclosure; Fig 3; 54pp; English.
CC The sequences given in R41990-2013 are mutant versions of the
CC Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants
CC generated by random mutation by PCR, may be used to modify the T-cell
CC response elicited by an antigen, by interacting with specific Vbeta
CC elements of the T-cell receptors. This T-cell response modulation
CC may be useful in a wide variety of autoimmune diseases, where self-
CC reactive T-cells may be activated by SAg that bind to particular
CC Vbeta types.
SQ Sequence 190 AA;
Query Match 43.0%; Score 758; DB 1; Length 190;
Best Local Similarity 58.9%; Pred. No. 7.29e-55;
Matches 112; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

DB 1 ESOPDPKDELHKSSKFTGLMENKVLVDNHNVAIVKSIDOFLYFDLYISIKDTKLG 60
1 ESOPDPKDELHKSSKFTGLMENKVLVDNHNVAIVKSIDOFLYFDLYISIKDTKLG 60
QY
DB 61 YDNVRFEFKKNLDADKKYKDYVDFGANYYYQCYFSNNNNNNNNNNNNNNNNNNNN 120
61 YDNVRFEFKKNLDADKKYKDYVDFGANYYYQCYFSKKTNDINSHEDKRTCTMGVTE 120
QY
DB 121 NNN 180
121 HNGNQLDKYSITVRFEDGKNLSPDVGQTKKVTQAQELDYLRHYLVKKKLYEFNNS 180
QY
DB 181 NNNNNNIKFI 190
181 PYETGYIKFI 190
QY 181 PYETGYIKFI 190

RESULT 11
ID R42012 standard; protein; 190 AA.
AC R42012;
DT 21-APR-1994 (first entry)
DE Staphylococcus enterotoxin B mutant BA-72.
KM Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
KM random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
KM autoimmune disease.
OS Staphylococcus aureus.
FH Key
FT Location/Qualifiers
FT 97..157
FT /note-"Region undisclosed in the specification"
FT 162..186
FT /note-"Region undisclosed in the specification"
FT region
FT WO9314634-A.
PD 05-AUG-1993.
PD 28-JAN-1993. U00839.
PR 28-JAN-1992; US-827540.
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
PI Kappeler JW, Marrack P;
DR WPI; 93-320314/40.

PT Preventing or treating toxic effects of super antigens - by admin. of
PT new modified or mutated super antigen which induces antibodies but
PT not T-cell activation
PS Disclosure; Fig 3; 54pp; English.
CC The sequences given in R41990-2013 are mutant versions of the
CC Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants
CC generated by random mutation by PCR, may be used to modify the T-cell
CC response elicited by an antigen, by interacting with specific Vbeta
CC elements of the T-cell receptors. This T-cell response modulation
CC may be useful in a wide variety of autoimmune diseases, where self-
CC reactive T-cells may be activated by SAg that bind to particular
CC Vbeta types.
SQ Sequence 190 AA;
Query Match 42.9%; Score 756; DB 1; Length 190;
Best Local Similarity 58.9%; Pred. No. 1.09e-54;
Matches 112; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

DB 1 ESOPDPKDELHKSSKFTGLMENKVLVDNHNVAIVKSIDOFLYFDLYISIKDTKLG 60
1 ESOPDPKDELHKSSKFTGLMENKVLVDNHNVAIVKSIDOFLYFDLYISIKDTKLG 60
QY
DB 61 YDNVRFEFKKNLDADKKYKDYVDFGANYYYQCYFSNNNNNNNNNNNNNNNNNNNN 120
61 YDNVRFEFKKNLDADKKYKDYVDFGANYYYQCYFSKKTNDINSHEDKRTCTMGVTE 120
QY
DB 121 NNN 180
121 HNGNQLDKYSITVRFEDGKNLSPDVGQTKKVTQAQELDYLRHYLVKKKLYEFNNS 180
QY
DB 181 NNNNNNIKFI 190
181 PYETGYIKFI 190
QY 181 PYETGYIKFI 190

RESULT 12
ID R41993 standard; protein; 190 AA.
AC R41993;
DT 21-APR-1994 (first entry)
DE Staphylococcus enterotoxin B mutant BR-291.
KM Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
KM random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
KM autoimmune disease.
OS Staphylococcus aureus.
FH Key
FT Location/Qualifiers
FT 97..157
FT /note-"Region undisclosed in the specification"
FT 162..186
FT /note-"Region undisclosed in the specification"
FT region
FT WO9314634-A.
PD 05-AUG-1993.
PD 28-JAN-1993. U00839.
PR 28-JAN-1992; US-827540.
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
PI Kappeler JW, Marrack P;
DR WPI; 93-320314/40.
PT Preventing or treating toxic effects of super antigens - by admin. of
PT new modified or mutated super antigen which induces antibodies but
PT not T-cell activation
PS Disclosure; Fig 3; 54pp; English.
CC The sequences given in R41990-2013 are mutant versions of the
CC Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants
CC generated by random mutation by PCR, may be used to modify the T-cell
CC response elicited by an antigen, by interacting with specific Vbeta
CC elements of the T-cell receptors. This T-cell response modulation
CC may be useful in a wide variety of autoimmune diseases, where self-
CC reactive T-cells may be activated by SAg that bind to particular
CC Vbeta types.
SQ Sequence 190 AA;
Query Match 42.9%; Score 756; DB 1; Length 190;
Best Local Similarity 58.9%; Pred. No. 1.09e-54;
Matches 112; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

Db 1 ESQPDPRPELHSSKFTGLMESMKVLYDNDHVSAINVKSIDQFLYFDLYSIKDKTLGN 60
OY 1 ESQPDPRPELHSSKFTGLMESMKVLYDNDHVSAINVKSIDQFLYFDLYSIKDKTLGN 60
Db 61 YDVRVREFKKNKDLADYKDKYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
OY 61 YDVRVREFKKNKDLADYKDKYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
Db 121 NNN 180
OY 121 HNGNQDLKYSITVRVFEDEKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Db 181 NNNNNNNIKFI 190
OY 181 PYETGYIKFI 190

RESULT 13
ID R41996 standard; protein; 190 AA.
AC R41996;
DT 21-APR-1994 (first entry)
DE Staphylococcus enterotoxin B mutant BC-88.
KW Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
KW random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
KW autoimmune disease.
OS Staphylococcus aureus.
FH key Location/Qualifiers
FT region 97..157
FT /note= "Region undisclosed in the specification"
FT 162..186
FT /note= "Region undisclosed in the specification"
PD MO9314634-A.
PN 05-AUG-1993.
PR 28-JAN-1992; US-827340.
PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
PI Kappler JW, Marrack P;
DR MPI; 93-320314/40.
PT Preventing or treating toxic effects of super antigens - by admin. of
PT new modified or mutated super antigen which induces antibodies but
PT not T-cell activation
PS Disclosures; Fig 3; 54pp; English.
CC The sequences given in R41990-2013 are mutant versions of the
CC Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants
CC generated by random mutation by PCR, may be used to modify the T-cell
CC response elicited by an antigen, by interacting with specific Vbeta
CC elements of the T-cell receptors. This T-cell response modulation
CC may be useful in a wide variety of autoimmune diseases, where self-
CC reactive T-cells may be activated by SAg that bind to particular
CC Vbeta types.
SQ Sequence 190 AA;

Query Match 42.9%; Score 756; DB 1; Length 190;
Best Local Similarity 58.9%; Pred. No. 1.09e-54;
Matches 112; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

Db 1 ESQPDPRPELHSSKFTGLMESMKVLYDNDHVSAINVKSIDQFLYFDLYSIKDKTLGN 60
OY 1 ESQPDPRPELHSSKFTGLMESMKVLYDNDHVSAINVKSIDQFLYFDLYSIKDKTLGN 60
Db 61 YDVRVREFKKNKDLADYKDKYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
OY 61 YDVRVREFKKNKDLADYKDKYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
Db 121 NNN 180
OY 121 HNGNQDLKYSITVRVFEDEKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Db 181 NNNNNNNIKFI 190
OY 181 PYETGYIKFI 190

RESULT 14
ID R41992 standard; protein; 190 AA.
AC R41992;
DT 21-APR-1994 (first entry)
DE Staphylococcus enterotoxin B mutant BR-257.
KW Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
KW random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
KW autoimmune disease.
OS Staphylococcus aureus.
FH key Location/Qualifiers
FT region 97..157
FT /note= "Region undisclosed in the specification"
FT 162..186
FT /note= "Region undisclosed in the specification"
PD MO9314634-A.
PN 05-AUG-1993.
PR 28-JAN-1992; US-827540.
PA (NAME-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
PI Kappler JW, Marrack P;
DR MPI; 93-320314/40.
PT Preventing or treating toxic effects of super antigens - by admin. of
PT new modified or mutated super antigen which induces antibodies but
PT not T-cell activation
PS Disclosures; Fig 3; 54pp; English.
CC The sequences given in R41990-2013 are mutant versions of the
CC Staphylococcus enterotoxin B (SEB) super antigen (SAg). These mutants
CC generated by random mutation by PCR, may be used to modify the T-cell
CC response elicited by an antigen, by interacting with specific Vbeta
CC elements of the T-cell receptors. This T-cell response modulation
CC may be useful in a wide variety of autoimmune diseases, where self-
CC reactive T-cells may be activated by SAg that bind to particular
CC Vbeta types.
SQ Sequence 190 AA;

Query Match 42.8%; Score 755; DB 1; Length 190;
Best Local Similarity 58.4%; Pred. No. 1.34e-54;
Matches 111; Conservative 31; Mismatches 48; Indels 0; Gaps 0;

Db 1 ESQPDPRPELHSSKFTGLMESMKVLYDNDHVSAINVKSIDQFLYFDLYSIKDKTLGN 60
OY 1 ESQPDPRPELHSSKFTGLMESMKVLYDNDHVSAINVKSIDQFLYFDLYSIKDKTLGN 60
Db 61 YDVRVREFKKNKDLADYKDKYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
OY 61 YDVRVREFKKNKDLADYKDKYVDFGANYYYOCYFSNNNNNNNNNNNNNNNNNNNNNN 120
Db 121 NNN 180
OY 121 HNGNQDLKYSITVRVFEDEKNLSPDYQTNKKKVTAAQELDYLTRHYLVKKNKLYEFNNS 180
Db 181 NNNNNNNIKFI 190
OY 181 PYETGYIKFI 190
RESULT 15
ID R42000 standard; protein; 190 AA.
AC R42000;
DT 21-APR-1994 (first entry)
DE Staphylococcus enterotoxin B mutant BA-15.
KW Staphylococcus; enterotoxin B; SEB; super antigen; SAg; receptor;
KW random mutation; PCR; modify; T-cell; response; antigen; Vbeta element;
KW autoimmune disease.
OS Staphylococcus aureus.
FH key Location/Qualifiers
FT region 97..157
FT /note= "Region undisclosed in the specification"
FT 162..186
FT /note= "Region undisclosed in the specification"
PD MO9314634-A.
PN 05-AUG-1993.

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Apr 20 15:08:07 2000; MasPar time 15.27 Seconds
 Tabular output not generated. 467,552 Million cell updates/sec

Title: >US-09-150-947-12
 Description: (1-239) from US09150947.pep
 Perfect Score: 1763
 Sequence: 1 ESQPPDKPDELHKSSKFTGL.....NKAVDSKDKVIEVLTTKKK 239

Scoring table:
 PAM 150
 Gap 11

Searched: 82229 segs, 29864866 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 47.318; Variance 95.221; scale 0.497

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1760	99.8	266	1	ETXB_STPAU ENTEROTOXIN TYPE B PRE	0.00e+00
2	1183	67.1	266	1	ETC1_STPAU ENTEROTOXIN TYPE C-1 P	1.67e-210
3	1156	65.6	266	1	ETC3_STPAU ENTEROTOXIN TYPE C-3 P	6.66e-205
4	1148	65.1	266	1	ETC2_STPAU ENTEROTOXIN TYPE C-2 P	3.03e-203
5	746	42.3	251	1	SPEA_STRPY EXOTOXIN TYPE A PRECUR	1.08e-120
6	412	23.4	258	1	ETXD_STPAU ENTEROTOXIN TYPE D PRE	2.16e-54
7	375	21.3	257	1	ETXA_STPAU ENTEROTOXIN TYPE A PRE	2.53e-47
8	329	18.7	257	1	ETXE_STPAU ENTEROTOXIN TYPE E PRE	1.15e-38
9	165	9.4	235	1	SPEC_STRPY EXOTOXIN TYPE C PRECUR	6.04e-10
10	112	6.4	517	1	CP5H_CANTR CYTOCHROME P450 52A8 (3.24e-02
11	105	6.0	796	1	DECI_YEAST DECI PROTEIN (MDM2 PR	2.56e-01
12	106	6.0	1328	1	YME4_YEAST TRANSPOSON TY1 PROTEIN	1.92e-01
13	106	6.0	1328	1	YMD0_YEAST TRANSPOSON TY1 PROTEIN	1.92e-01
14	106	6.0	1347	1	YCB9_YEAST TRANSPOSON TY1-17 PROT	2.56e-01
15	105	6.0	1347	1	YCB9_YEAST TRANSPOSON TY1 PROTEIN	1.92e-01
16	106	6.0	1755	1	YU29_YEAST TRANSPOSON TY1 PROTEIN	2.56e-01
17	105	6.0	1755	1	YU29_YEAST TRANSPOSON TY1 PROTEIN	2.56e-01
18	104	5.9	638	1	GLE_CHLRE AUTOLYSIN PRECURSOR (E	3.42e-01
19	104	5.9	722	1	Y290_HAINE PROBABLE CARION-TRANS	3.42e-01
20	104	5.9	1328	1	YMT5_YEAST TRANSPOSON TY1 PROTEIN	3.42e-01
21	104	5.9	1409	1	COMI_DROME COPIA PROTEIN.	3.42e-01
22	102	5.8	342	1	YMI2_YEAST HYPOTHETICAL 39.2 KD P	6.05e-01
23	103	5.8	500	1	Y039_BORBU HYPOTHETICAL PROTEIN B	4.55e-01

24	102	5.8	776	1	ARCB_ECOLI AEROBIC RESPIRATION CO	6.05e-01
25	103	5.8	918	1	CAPB_CORGL PHOSPHOENOLPYRUVATE CA	4.55e-01
26	98	5.6	131	1	SP27_CABEL SPERMATOCYTE PROTEIN S	1.85e+00
27	99	5.6	321	1	VG16_BPB03 ENCAPSIDATION PROTEIN	1.40e+00
28	97	5.5	404	1	TY3H_CABEL PUTATIVE TYROSINE 3-MO	2.43e+00
29	97	5.5	605	1	ETFI_FOMP1 EARLY TRANSCRIPTION FA	2.43e+00
30	97	5.5	682	1	REGC_BACSU ATP-DEPENDENT DNA HELI	2.43e+00
31	97	5.5	710	1	PAL3_PHAUV PHENYLALANINE AMMONIA-	2.43e+00
32	97	5.5	2090	1	N214_HUMAN NUCLEAR PORE COMPLEX P	2.43e+00
33	97	5.5	2314	1	PTP2_HUMAN PROTEIN-TYROSINE PHOSP	2.43e+00
34	96	5.4	666	1	VOO1_VARV PROTEIN O1.	3.19e+00
35	95	5.4	1476	1	CFTP_MOUSE CYSTIC FIBROSIS TRANSM	4.18e+00
36	96	5.4	2316	1	PTP2_RAT PROTEIN-TYROSINE PHOSP	3.19e+00
37	94	5.3	464	1	GATH_YEAST PROBABLE GLUTAMYL-TRNA	5.45e+00
38	94	5.3	519	1	CP50_CANMA CYTOCHROME P450 52A10	5.45e+00
39	94	5.3	519	1	CP5K_CANMA HYPOHETICAL 63.9 KD P	7.11e+00
40	93	5.3	560	1	YUK5_YEAST PROTEIN-TYROSINE PHOSP	7.11e+00
41	93	5.3	700	1	PTPE_HUMAN HYPOHETICAL 63.9 KD P	7.11e+00
42	94	5.3	971	1	PTPE_HUMAN HYPOHETICAL 63.9 KD P	7.11e+00
43	94	5.3	986	1	PTPE_HUMAN HYPOHETICAL 63.9 KD P	7.11e+00
44	94	5.3	1476	1	PTPE_HUMAN HYPOHETICAL 63.9 KD P	7.11e+00
45	93	5.3	1682	1	MSPI_PLAF3 MEROZOITE SURFACE PROT	7.11e+00

ALIGNMENTS

RESULT ID	1	STANDARD:	PRT:	266 AA.
AC	ETXB_STPAU			
DT	P01552;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	ENTEROTOXIN TYPE B PRECURSOR (SEB).			
GN	ENTB.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
CC	Bacillus/staphylococcus group; Staphylococcus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 86168029.			
RA	JONES C.L., KHAN S.A.;			
RT	"Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.";			
RL	J. Bacteriol. 166:29-33(1986).			
RN	[2]			
RP	SEQUENCE OF 40-91 FROM N.A.			
RX	MEDLINE: 85298255.			
RA	RANELLI D.M., JONES C.L., JOHNS M.B., MUSSEY G.J., KHAN S.A.;			
RT	"Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).			
RN	[3]			
RP	SEQUENCE OF 28-266 (S-6).			
RX	MEDLINE: 71007902.			
RA	HUANG I.-Y., BERGDOHL M.S.;			
RT	"The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";			
RL	J. Biol. Chem. 245:3518-3525(1970).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).			
RX	MEDLINE: 93063291.			
RA	SWAMINATHAN S., FOREY W.F., JR., PLETCHER J., SAX M.;			
RT	"Crystal structure of staphylococcal enterotoxin B, a superantigen.";			
RL	Nature 359:801-806(1992).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.			
RX	MEDLINE: 94203282.			
RA	JARETZKY T.S., BROWN J.H., GORCA J.C., STERN L.J., URBAN R.G.,			
RT	CHI Y.I., STAUFFACHER C., STROMINGER J.L., WILEY D.C.;			
RL	"Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";			
RL	Nature 368:711-718(1994).			

[6]
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RP MEDLINE: 99096298.
RA LI H., LIERA A., TSUCHIYA D., LEDER L., YSERN X., SCHLIEVERT P.M.,
RA KARJALAINEN K., MARIUTZA R.A.,
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
RN 177
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE: 98181012.
RA PAPAGEORGIOU A.C., TRANTER H.S., ACHARYA K.R.,
RT Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC -----
CC DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
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CC -----
CC EMBL: M1118; AAA8550.1; -.
DR PIR: A01815; ENSAB6.
DR PIR: S27360; S27360.
DR PDB: 1SEB; 20-JUN-96.
DR PDB: 2SEB; 28-JAN-98.
DR PDB: 3SEB; 27-MAY-98.
DR PDB: 1SE3; 16-JUN-97.
DR PDB: 1SE4; 15-OCT-97.
DR PDB: 1SBB; 04-MAR-99.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; STAPH_STREP_TOXIN; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
SQ SEQUENCE 266 AA; 31436 MW; E2C09D63 CRC32;
Query Match 99.8%; Score 1760; DB 1; Length 266;
Best Local Similarity 99.6%; Pred. No. 0.00e+00;
Matches 238; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 208 PYETGYIKFIENENSWFWDMPAPGDKFDSQSKYLMYNDKMKVSKDKVILEVLTTRKK 266
OY 181 PYETGYIKFIENENSWFWDMPAPGDKFDSQSKYLMYNDKMKVSKDKVILEVLTTRKK 239
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ID ETC1_STAUB STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-1 PRECURSOR (SECI).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88038352.
RA BOHACH G.A., SCHLIEVERT P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE: 83213327.
RA SCHMIDT J.J., SPERO L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X05815; CAA29260.1; -.
DR PIR: A01816; ENSAC1.
DR PIR: S06356; S06356.
DR HSSP: P34071; 1SE2.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; STAPH_STREP_TOXIN; 1.
KW Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266
FT DISULFID 120 137
FT CONFLICT 177 177
SQ SEQUENCE 266 AA; 30546 MW; FE00255A CRC32;
Query Match 67.1%; Score 1183; DB 1; Length 266;
Best Local Similarity 66.8%; Pred. No. 1.67e-210;
Matches 161; Conservative 40; Mismatches 34; Indels 6; Gaps 6;

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OY 179 NSPYETGYIKFTIENE-NSFWYDMMPAPGDKFPQSKYLMYNDNKVDSKDVXIEVYLTFR 237
DB 265 N 265
OY 238 K 238

RESULT 3
ID ETC3_STAU STANDARD: PRT: 266 AA.
AC P2313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-3 PRECURSOR (SEC3).
GN ENTC3.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90220508.
RA HOVDE C.J., HACKETT S.P., BOHACH G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins."
RL Mol. Gen. Genet. 220:329-333(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH T-CELL RECEPTOR.
RX MEDLINE: 97064178.
RA FIELDS B.A., MALCHIODI E.L., LI H., YSEHN X., STAUFACHER C.V.,
RA SCHLIEVERT P.M., KARJALAINEN K., MARIUZZA R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen."
RL Nature 384:188-192(1996).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PROGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X51661; CAA35972.1; -.
DR PIR: S11885; S11885.
DR PDB: 1JCK; 12-NOV-97.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFMW: PF01123; Staph_strep_toxin; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137 BY SIMILARITY.
FT SEQUENCE 266 AA; 30671 MW; 27B4DD0A CRC32;
SQ

Query Match 65.6%; Score 1156; DB 1; Length 266;
Best Local Similarity 66.0%; Pred. No. 6,66e-205;
Matches 135; Conservative 40; Mismatches 36; Indels 6; Gaps 6;

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OY 121 HNGNQLDK-Y-RSIVRVFEDSKNLISFVQYTNKKKVTQGEJLYLRHLVANKKRIEEN 178
DB 205 SSPYETGYIKFTIENNGNFTWYDMMPAPGDKFPQSKYLMYNDNKVDSKSVXIEVHLLTK 264
OY 179 NSPYETGYIKFTIENE-NSFWYDMMPAPGDKFPQSKYLMYNDNKVDSKDVXIEVYLTFR 237
DB 265 N 265
OY 238 K 238

RESULT 4
ID ETC3_STAU STANDARD: PRT: 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE C-2 PRECURSOR (SEC2).
GN ENTC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE: 89277549.
RA BOHACH G.A., SCHLIEVERT P.M.;
RT "Conservation of the biologically active portions of staphylococcal
RT enterotoxins C1 and C2."
RL Infect. Immun. 57:2249-2252(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE: 96027099.
RA PAPAGEORGIOU A.C., ACHARYA K.R., SHAPIRO R., PASSALACQUA E.F.,
RA BREHM R.D., TRANTER H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
RT staphylococcus aureus reveals a zinc-binding site."
RL Structure 3:769-779(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE: 96022987.
RA SWAININTHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE: 9734373.
RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., ACHARYA K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PROGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
DR PIR: A60114; A60114.
DR PDB: 1SE2; 08-MAR-96.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFMW: PF01123; Staph_strep_toxin; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Zinc; 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
SQ SEQUENCE 266 AA; 30604 MW; A15FD37 CRC32;

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Query Match          65.1%; Score 1148; DB 1; Length 266;
Best Local Similarity 65.6%; Pred. No. 3,036-203;
Matches 158; Conservative 40; Mismatches 37; Indels 6; Gaps 6;

Db 28 ESQDPDPDELHKSSSEFGTGMNKKYLVDHYVATKMSVSKFLADLIYNISDKLKN 87
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1 ESQDPDPDELHKSSSEFGTGMNKKYLVDHYVATKMSVSKFLADLIYNISDKLKN 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      88 YDKKTELLNEDLAKKRYKDEVDVYGSNYVNCYFSSK-DNV-GKVYGG-RTCMYGGITK 144
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      61 YDNVREKKNKDLADKYDKYVDVFGANYVYOCYFSKKTNDINSHEITKRTCMGVTE 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      145 HEGNHFDMGNLQNLVIRYENKRTISEVOTDKRSVTAQELDKARFLINKKNLYEFN 204
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      121 HNGQDLK-Y-RSITVRFEDEGKNLSFDVOTNKKVTAQELDYLTRHYLVKNNKLYEFN 178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      205 SSPETGYIKFIENNGNTFTYDMPAPGDKDQSKYLMYNDKNTVDSKSVKIEVHLTK 264
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      179 NSPYETGYIKFIENE-NSFWYDMPAPGDKDQSKYLMYNDKNTVDSKSVKIEVHLTK 237
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 265 N 265
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      238 K 238

RESULT 5
ID SPEA_STRPY STANDARD; PRT; 251 AA.
AC P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EXOTOXIN TYPE A PRECURSOR (SCARLET FEVER TOXIN) (ERYTHROGENIC TOXIN)
DE (SPE A).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86166804.
RA WEEKS C.R., FERRETTI J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12."
RN [2]
RL Infect. Immun. 52:144-150(1986).
RP SEQUENCE FROM N.A.
RX MEDLINE; 86284313.
RA JOHNSON L.P., L'ITALIEN J.J., SCHLIEVERT P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B."
RL Mol. Gen. Genet. 203:354-356(1986).
CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC FEVER.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----
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CC -----
CC CC EMBL; U04053; AAC48868.1; -
CC DR EMBL; X03929; CA27568.1; -
CC DR PIR; A26152; A26152.
CC PIR; S29659; S29659.

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DR HSSP; P01552; 1SEB.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph-Strep-toxin; 1.
DR Toxin; Signal.
KW SIGNAL.
FT 1 30
FT CHAIN 31 251
FT CONFLICT 6 6
FT CONFLICT 17 18
FT CONFLICT 25 35
FT CONFLICT 40 40
FT CONFLICT 43 43
FT CONFLICT 47 59
FT CONFLICT 129 129
FT CONFLICT 165 178
SQ SEQUENCE 251 AA; 29246 MW; 535FE465 CRC32;
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      30 AQODPDSQLHRSSTLVKNL-QNIFYLYEGDPTVENKSVQDLSDLIYVNSGP---NY 85
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      2 SQDPKPKDELHKSSSEFGTGMNKKYLVDHYVATKMSVSKFLADLIYNISDKLKN 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      86 DKLTELKNOEMATLFDKNDVIGVEYHLCTLC---E-NA-E---RSACIGCYTNH 136
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      62 DNVRFEKKNKDLADKYDKYVDVFGANYVYOCYFSKKTNDINSHEITKRTCMGVTEH 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      137 EGNHLEIPKRIYVKSISDQSLSPDIETNKKVTAQELDYKVRKYLTDNKLQYTNQPSK 196
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      122 NGNQLDKRSTIVRYEFGKNLSFDVOTNKKVTAQELDYLTRHYLVKNNKLYEFN 181
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      197 YETGYIKFIENKSEFWDFPEP-E-FTQSKYLMYKNDLTDLSNTSQIEVYLTTK 251
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      182 YETGYIKFI-ENNSFWYDMPAPGDKDQSKYLMYNDKNTVDSKSVKIEVYLTTK 237
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
ID ERYD_STAUV STANDARD; PRT; 238 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ENTEROTOXIN TYPE D PRECURSOR (SED).
GN ENTND.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89359112.
RA BAYLES K.W., IANDOLO J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal
RT enterotoxin D."
RL J. Bacteriol. 171:4799-4806(1989).
RN [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN-ATCC 23235;
RX MEDLINE; 97157473.
RA SUNDSTROM M., ABRAHMSSEN L., ANTONSSON P., MEHINDATE K., MOURAD W.,
RA DOHLSTEN M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals
RT zn2+-mediated homodimerization."
RL EMBO J. 15:6832-6840(1996).
CC -1- SUBUNIT: HOMODIMER; ZINC-DEPENDENT.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S.AUREUS ENTEROTOXINS AND S.PYOGENES
CC PYROGENIC EXOTOXINS ARE ALL RELATED.
CC -----

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[illegible]

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RT "Crystal structure of the superantigen staphylococcal enterotoxin
RL type A." ;
RN EMBL J. 14:3292-3301(1995).
RX [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RA MEDLINE; 97113025.
RX SUNDSTROM M., HALLEN D., SVENSSON A., SCHAD E., DOHLSTEIN M.,
RA ABRAHAMSEN L.;
RT "The Co-crystalline structure of staphylococcal enterotoxin type A with
RT zeta+ at 2.7-A resolution. Implications for major histocompatibility
RT complex class II binding.";
RL J. Biol. Chem. 271:32212-32216(1996).
RN [5]
RP 3D-STRUCTURE MODELING.
RX MEDLINE; 96022987.
RA SAMMATHAN S., FUREY W.F. JR., PLETCHER J., SAX M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins." ;
RL Nat. Struct. Biol. 2:680-686(1995).
RN [6]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE; 97334373.
RA SCHAD E.M., PAPAGEORGIOU A.C., SVENSSON L.A., AGHARRA K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity." ;
RL J. Mol. Biol. 269:270-280(1997).
CC -1- SUBUNIT: MONOMER.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYOGENIC EXOTOXINS ARE ALL RELATED.
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CC -----
DR EMBL; M18970; AAA26681.1; -.
DR PIR; A28664; A28664.
DR PIR; A29566; A29566.
DR PID; ISEF; 11-JUL-96.
DR PDB; 1SEA; 15-OCT-95.
DR PDB; 1SXT; 19-NOV-97.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM; PF01123; Staph_Strep_toxin; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; zinc; 3d-structure.
FT SIGNAL 1 24
FT CHAIN 25 237 ENTEROTOXIN TYPE A.
FT DISULFID 120 130
FT METAL 25 25 ZINC.
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT CONFLICT 242 242 T -> S (IN REF. 2).
SQ SEQUENCE 257 AA; 29669 MW; D08631B2 CRC32;

Query Match 21.3%; Score 375; DB 1; Length 257;
Best Local Similarity 35.0%; Pred. No. 2.55e-47;
Matches 82; Conservative 56; Mismatches 77; Indels 19; Gaps 12;

Db 35 DARKSELGATGLNLKQIYYNEKAKTENKESHQDFQHTLFKEGFETHSWYNLDLV 94
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 10 ELHNSKKTGL-MEMNK-VLYDDNHVSALNKSIDLQFLYPLDIISINDTKGNDDNRVE 67
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 95 FDSADIYDKIKKKVVDLYGAYGYQC-----AGG--T'-PNA-TACMGVTLHDNNRLT 144
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Oy 68 FKNDYDKDYDVVDYGANYCYCFYSKKTNDINSHTKRTCKMGVTEHNGLD 127

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Db      145 EKKKVPINLMDGKONTVPLETVTKNNKNVTVOELDLQARRLYOEKYNLYNSDVPDGKQ 204
      : : : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Oy      128 KXSTIVRVPEDECK-NLSPD-VQTNKKKTTAQLDLVLRHLYLVKKKKLYEFNN-NSPYE 183
      : : : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Db      205 RGLIVHSTEPSVNYDLFGAOGQ-YSMT-LRIRYDNKNTINSENMHIDLYLT 256
      : : : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Oy      184 TGXIKF-IENENEFWYDMPAPGDKFDQSKYLMWYNDKNKVDKIVIEYLYTT 236
      : : : : | | | : : : | | | | | | | | | | : : : : : : : : : :

RESULT  8
ID      ETRX-STRAU      STANDARD;      PRT;      257 AA.
AC      P13993;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      ENTEROTOXIN TYPE E PRECURSOR (SEE).
GN      ENTE.
OS      Staphylococcus aureus.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
RN      Bacillus/staphylococcus group; Staphylococcus.
RP      [1]
RC      SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC      STRAIN-MJB265;
RX      MEDLINE; 88257005.
RA      COUCH J.L., SOLTIS M.T., BETLEY M.J.;
RT      "Cloning and nucleotide sequence of the type E staphylococcal
RT      enterotoxin gene.";
RL      J. Bacteriol. 170:2954-2960(1988).
RN      [2]
RP      3D-STRUCTURE MODELING.
RX      MEDLINE; 96022987.
RA      SWAMINATHAN S., FUREY M.F., JR., PLETCHER J., SAX M.;
RT      "Residues defining V beta specificity in staphylococcal
RT      enterotoxins.";
RL      Nat. Struct. Biol. 2:680-686(1995).
CC      -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC      STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC      -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC      PYROGENIC EXOTOXINS ARE ALL RELATED.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M21319; AAA26617.1; -.
DR      PIR; A28179; A28179.
DR      PDB; 1SEB; 15-OCT-95.
DR      PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR      PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR      PFAM; PF01123; Staph_Strep_toxin; 1.
KW      Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT      SIGNAL 1 27
FT      CHAIN 28 257 ENTEROTOXIN TYPE E.
SO      SEQUENCE 257 AA; 29358 MW; 88BA67C3 CRC32;

Query Match 18.7%; Score 329; DB 1; Length 257;
Best local Similarity 33.8%; Pred. No. 1,15e-38;
Matches 79; Conservative 56; Mismatches 80; Indels 19; Gaps 13;

Db      35 DLKKSELDQNALSLNRQIYYNEKAITENKESDDOFLENTLLFKGFTGHPMYNDLVD 94
      : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Oy      10 ELHKSSKFT-GLMENMK-VLYDDNHSAIVKSIDQFLYDLIYSKDTLGYNDVRYVE 67
      : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Db      95 LGSKDKATNKKKKGVLDLYGAYGYQC-----AGS--T--PNK-TACHTGYVTLDHNNRLT 144
      : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Oy      68 FKKRLADAKYKDYVYVGFANYCYFYSKKTNDINSHTDKRRTCTGYGVTEHNGQDLD 127
      : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Db      145 EKKKVPINLMDGKONTVPIDKVTSKKEVTQVELDLQARRHYLHGKFGLYLNSDPSFGKQV 204

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Oy      128 KXSTIVRVPEDECKNL-LSPD-VQTNKKKTTAQLDLVLRHLYLVKKKKLYEFNN-SP-YE 183
      : : : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Db      205 RGLIVHSSGSESVSYDLFGAOGQ-YPDT-LRIRYDNKNTINSENMHIDLYLT 256
      : : : : | | | : : : | | | | | | | | | | : : : : : : : : : :
Oy      184 TGXIKFIEENENS-FWYDMPAPGDKFDQSKYLMWYNDKNKVDKIVIEYLYTT 236
      : : : : | | | : : : | | | | | | | | | | : : : : : : : : : :

RESULT  9
ID      SPEC-STREPY      STANDARD;      PRT;      235 AA.
AC      P13380;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      EXOTOXIN TYPE C PRECURSOR (SPE C).
GN      SPEC.
OS      Streptococcus pyogenes.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
RN      Streptococcus.
RP      [1]
RC      SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.
RC      STRAIN-T18P / MGAS 1585;
RX      MEDLINE; 88314303.
RA      GOSHORN S.C., SCHLIEVERT P.M.;
RT      "Nucleotide sequence of streptococcal pyrogenic exotoxin type C.";
RL      Infect. Immun. 56:2518-2520(1988).
RN      [2]
RP      REVISIONS TO 21-26.
RC      STRAIN-T18P / MGAS 1585;
RX      MEDLINE; 92363541.
RA      KAPUR V., NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT      "Molecular population genetic evidence of horizontal spread of two
RT      alleles of the pyrogenic exotoxin C gene (spec) among pathogenic
RT      clones of Streptococcus pyogenes.";
RL      Infect. Immun. 60:3513-3517(1992).
RN      [3]
RP      X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
RX      MEDLINE; 97397352.
RA      ROUSSEL A., ANDERSON B.F., BAKER H.M., FRASER J.D., BAKER E.N.;
RT      "Crystal structure of the streptococcal superantigen SPE-C:
RT      dimerization and zinc binding suggest a novel mode of interaction
RT      with MHC class II molecules.";
RL      Nat. Struct. Biol. 4:635-643(1997).
CC      -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
CC      THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC      FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC      DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC      FEVER.
CC      -----
CC      -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC      -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC      PYROGENIC EXOTOXINS ARE ALL RELATED.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M35514; AAA27017.1; ALT_SEQ.
DR      EMBL; M97156; AAB59091.1; -.
DR      EMBL; M97157; AAB59092.1; -.
DR      PIR; A30509; A30509.
DR      PDB; 1AN8; 29-APR-98.
DR      PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR      PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR      PFAM; PF01123; Staph_Strep_toxin; 1.
KW      Toxin; Signal; 3D-structure.
FT      SIGNAL 1 27
FT      CHAIN 28 235 EXOTOXIN TYPE C.
SO      SEQUENCE 235 AA; 27372 MW; 524BB55D CRC32;

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Query Match 9.4%: Score 165; DB 1; Length 235;
Best Local Similarity 25.8%; Pred. No. 6, 04e-10;
Matches 32; Conservative 37; Mismatches 49; Indels 6; Gaps 6;

Db 113 IYGGITPAQNKRVN-HKLLGNLFISGESQOINNNKIIIEKDVDFQFQEDFKIRKYLMDNY 171
      :|||:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Qy 114 MGVTTEHNGNQLDKYRSI-TYRVEDKEDSLSPVQVQNKKKVYQVQEDLDLTRHLYVANK 172
      :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 172 KIYD-AISPPYVSGRIETKDKGHEQIDLFDSPNEG-TRSDIEAFYKDNRIITNMKFSFH 229
      :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Qy 173 KLYERNNSPYETGYIKFLENENSF-WYDMAMPDGDKFOOSKLYIMAYNNDKMYDSKD-VKI 230
      :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 230 DIYL 233
      :|||
Qy 231 EYVL 234

RESULT 10
ID CPH CANTR STANDARD: PRT: 517 AA.
AC P30610.
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 52A8 (BC 1.14.14.1) (CYPLI1A8) (ALKANE-INDUCIBLE P450-
DE AK5).
CS CYP52A8.
SN Candida tropicalis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Candidaceae; Candida.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 750;
RX MEDLINE: 93090274.
RA SEGHEZZI W., METILI C., RUFFINER R., KUENZLI R., SANGIARD D.,
RA FISCHTER A.;
RT "Identification and characterization of additional members of the
RT cytochrome P450 multigene family CYP2 of Candida tropicalis.";
RL DNA Cell Biol. 11:767-780(1992).
CC -1- FUNCTION: TOGETHER WITH AN NADPH CYTOCHROME P450 THE ENZYME SYSTEM
CC CATALYZES THE TERMINAL HYDROXYLATION AS THE FIRST STEP IN THE
CC ASSIMILATION OF ALKANES AND FATTY ACIDS. PREFERENTIALLY
CC HYDROXYLATES LAURIC ACID.
CC -1- CATALYTIC ACTIVITY: HYDROXYLATION OF N-ALKANES AT THE TERMINAL
CC POSITION.
CC -1- INDUCTION: BY VARIOUS ALKANES.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----
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CC -----
CC EMBL: Z13012; CAA78356.1; -.
CC DR PIR: S22974; S22974.
CC DR PROSITE: PS00086; CYTOCHROME_P450; 1.
CC DR PFAM: PF00067; P450; 1.
CC Electron transport; Oxidoreductase; Monooxygenase; Heme.
CC FM BINDING 464 464 HEME (BY SIMILARITY).
CC Kt SEQUENCE 517 AA; 59525 MW; D851204F CRC32;
Cc

Query Match 6.4%: Score 112; DB 1; Length 517;
Best Local Similarity 27.9%; Pred. No. 3, 24e-02;
Matches 17; Conservative 20; Mismatches 18; Indels 6; Gaps 5;

Db 189 FTVDSATEFLFGESVHSLKDETTGYSYDD-IDVGRKDPAESFNKAOEYLAIRTLVDFY 247
      :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Qy 36 INVKSIDQFLYFDLITKDKTGLGYNDVRYVEKN-KDLADKY-KDK-YVDV--EGANY 90
      :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:| :|:|:|
Db 248 Y 248
      |

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OY      91 Y 91

RESULT 11
ID      DECI YEAST        STANDARD;          PRT;       796 AA.
AC      012387;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      01-NOV-1997 (Rel. 35, Last annotation update)
DT      DECI PROTEIN (MDM20 PROTEIN).
GN      DECI OR MDM20 OR YOL076W.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
CC      Saccharomycetaceae; Saccharomyces.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      KINGSBURY T.J., HOYT M.A.;
RL      Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
RN      RN
RP      SEQUENCE FROM N.A.
RA      HERRMAN G.J., SHAW J.M.;
RL      Submitted (APR-1996) to the EMBL/Genbank/DDBJ databases.
RN      RN
RP      SEQUENCE FROM N.A..
RX      MEDLINE; 97321807.
RA      TZEEMIA M., KATSIOULOU C., ALEXANDRAKI D.;
RT      "Sequence analysis of a 3.2 kb segment from the left arm of yeast
RT      chromosome XV reveals eight known genes and ten new open reading
FR      frames including homologues of ABC transporters, Inositol
RT      phosphatases and human expressed sequence tags.";
RL      Yeast 13:583-589(1997).
CC      -I FUNCTION: GENETICALLY INTERACTS WITH CIN8.
-----
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-----
DR      EMBL; U36382; AAA79781.1; -.
DR      EMBL; U54799; AAB00196.1; -.
DR      EMBL; Z74818; CAAG9086.1; -.
DR      SCD; L00002975; DEC1.
SQ      SEQUENCE 796 AA; 92808 MW; C5OD7B42 CRC32;

Query Match      6.0%; Score 105; DB 1; Length 796;
Best Local Similarity 22.4%; Pred. No. 2,56e+01;
Matches 19; Conservative 24; Mismatches 36; Indels 6; Gaps 6;

Db      46 REFQSPGR-FDVKTKLEBPYGLKGTITGDPSLFLL-HNPFVELGK-YDEALHYVERGN 102
OY      128 KRSTRTVFEEFGKNML-SFDVOTKKKVTAOEELYLTRHLYVNKKKLKEFNNSPELTGY 186
         ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DY      187 IKFIENENSF-WYDMMPADGDKFDQ 210

RESULT 12
ID      YME4 YEAST        STANDARD;          PRT;       1328 AA.
AC      Q04711;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DE      15-DEC-1999 (Rel. 39, Last annotation update)
DT      TRANSPOSON TY1 PROTEIN B.
GN      TY1B OR YM1044W OR YM9827_08.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
CC      Saccharomycetaceae; Saccharomyces.
RN      [1]
RP      SEQUENCE FROM N.A.
```

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RC STRAIN-S288C / AB972;
RA ODELL C., BOWMAN S., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (JAN-1995) to the EMBL/GeneBank/DBJ databases.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL: Z47816; GAB87830.1; -
DR PROSITE: PS00141; ASP_PROTEASE; 1.
KW Transposable element; Hypothetical protein; Hydrolase;
KM Aspartyl protease; ATP-binding.
FT ACT SITE 34 34
FT NP BIND 1204 1211
FT SEQUENCE 1328 AA; 150945 MW; 17EA7E22 CRC32;
SO QUERY MATCH
Best Local Similarity 28.6%; Pred. No. 1,92e+01;
Matches 20; Conservative 23; Mismatches 25; Indels 2; Gaps 2;
Db 1009 LNANKKITTLKKQYDTRINIGESDNEIQDIL-GLEIKYRGKRYMKLGMSNLSITE-KI 1066
1 1111 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
168 LVKNKKLVFNNSPPEGYIKFEINENSFWDMPAPDKDPQSKYLMMYNDKMVKSD 227
Db 1067 PKLANPLPK 1076
1 : : : : :
228 VKIEVLYLTTK 237
Oy
RESULT 13
ID YMD9 YEAST STANDARD: PRT; 1328 AA.
AC 003434;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE TRANSPONIN TY1 PROTEIN B.
GN TY1B OR YML039W OR YM8054.04.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycos.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA CONNOR R., CHURCHER C., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (FEB-1995) to the EMBL/GeneBank/DBJ databases.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
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-----
DR EMBL: Z48430; GAB89330.1; -
DR PROSITE: PS00141; ASP_PROTEASE; 1.
KW Transposable element; Hypothetical protein; Hydrolase;
KM Aspartyl protease; ATP-binding.
FT ACT SITE 34 34
FT NP BIND 1204 1211
FT SEQUENCE 1328 AA; 151036 MW; F4A24298 CRC32;
SQ
Query Match
Best Local Similarity 28.6%; Pred. No. 1,92e+01;
Matches 20; Conservative 23; Mismatches 25; Indels 2; Gaps 2;
Db 1009 LNANKKITTLKKQYDTRINIGESDNEIQDIL-GLEIKYRGKRYMKLGMSNLSITE-KI 1066

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QY      168 LVKNNKILKEFNNSPPEETGYIKFIENENSFWDMMAPADKDFQDSKTYLMMYNDKNKMYDSKD 227
      Db      1067 PKLNVPLNPK 1076
      QY      228 VKIEVYLTWK 237

RESULT  14
ID      YMU0_YEAST      STANDARD:      PRT: 1328 AA.
AC      Q04670:
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-DEC-1999 (Rel. 39, Last annotation update)
DE      TRANSPOSON TY1 PROTEIN B.
GN      TY1B OR YMR050C OR YMR9796.03C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
      CC      Saccharomycetaceae; Saccharomyces.
      RN      [1]
      RP      SEQUENCE FROM N.A.
      RC      STRAIN-S288C / AB972;
      RA      DEVILIN K., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A.;
      RL      Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
      CC      -I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY U23.
      CC      -----
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      CC      or send an email to license@isb.sib.ch).
      CC      -----
      CC      EMBL: Z49703; CAA89760.1; '-'
      DR      PROSITE: PS00141; ASP_PROTEASE: 1.
      KW      Transposable element; Hypothetical protein; Hydrolase;
      KW      Aspartyl protease; ATP-binding.
      FT      ACT_SITE      34
      FT      NP_BIND      1204 1211      ATP (POTENTIAL).
      SQ      SEQUENCE      1328 AA; 150967 MW; BEDF3141 CRC32;

Query Match      6.0%; Score 106; DB 1; Length 1328;
Best Local Similarity 28.6%; Pred. No. 1,92e-01;
Matches 20; Conservative 23; Mismatches 25; Indels 2; Gaps 2;

Db      1009 LVNNKKITLTLLKKQDYTKINLGESEDNELQYDIL-GLEIKYRGKYMRLGMSNLSITE-KI 1066
      QY      168 LVKNNKILKEFNNSPPEETGYIKFIENENSFWDMMAPADKDFQDSKTYLMMYNDKNKMYDSKD 227
      Db      1067 PKLNVPLNPK 1076
      QY      228 VKIEVYLTWK 237

RESULT  15
ID      YCB9_YEAST      STANDARD:      PRT: 1347 AA.
AC      P25384:
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-MAY-1992 (Rel. 22, Last sequence update)
DT      15-DEC-1998 (Rel. 37, Last annotation update)
DE      TRANSPOSON TY1-17 PROTEIN B.
GN      TY1B OR YCL019W OR YCL19W.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
      CC      Saccharomycetaceae; Saccharomyces.
      RN      [1]
      RP      SEQUENCE FROM N.A.
      RC      MEDLINE: 86205247.
      RA      WASHINGTON J.R., ANNAR R., NEWLON C.S., WARING R.B., DAVIES R.W.,
      RA      INDGE K.J., OLIVER S.G.;
      RT      "A 'hot-spot' for Ty transposition on the left arm of yeast
      RT      chromosome III."
      RT      chromosome III."

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(TM)

MParch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 20 15:13:54 2000; Maspar time 17.90 Seconds
Tabular output not generated. 629.702 Million cell updates/sec

Title: >US-09-150-947-12
Description: (1-239) from US09150947.pep
Perfect Score: 1763
Sequence: 1 ESQDPKPEDELHKSKFTGL.....NKMWDKDVKIEVYLTTRKK 239

Scoring table:
PAM 150
Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r62
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 46.393; Variance 108.813; scale 0.426

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1760	99.8	266	1	ENSAB6 enterotoxin B precursor	2.96e-284
2	1183	67.1	266	1	ENSAC1 enterotoxin C-1 precu	1.19e-180
3	1156	65.6	266	2	S11885 enterotoxin C3 - Stap	7.73e-176
4	1148	65.1	266	2	A60114 enterotoxin C-2 precu	2.05e-174
5	746	42.3	251	1	S29659 exotoxin type A precu	1.75e-103
6	704	39.9	236	2	S18789 exotoxin A precursor	3.53e-96
7	694	39.4	236	2	S18783 exotoxin type A precu	1.92e-94
8	690	39.1	236	2	S18786 exotoxin type A precu	9.49e-94
9	598	33.9	250	1	A26152 streptococcal pyrogen	7.07e-78
10	412	23.4	258	2	A31953 enterotoxin D precursor	1.85e-46
11	375	21.3	257	2	A28664 enterotoxin A precursor	2.27e-40
12	373	21.2	253	2	A29566 enterotoxin A - Stap	4.82e-40
13	329	18.7	257	2	A28179 enterotoxin E precursor	6.51e-33
14	165	9.4	235	2	A30509 exotoxin C precursor	4.19e-08
15	117	6.6	509	2	D69832 probable Rheske [2Fe-	5.91e-02
16	117	6.6	592	2	C70108 peptidase homolog - L	5.91e-02
17	114	6.5	689	1	E70408 ferritin iron transport	1.32e-01
18	112	6.4	208	2	S72286 ribosomal protein S4	2.25e-01
19	112	6.4	517	2	S22974 cytochrome P450 52A8	2.25e-01
20	110	6.4	1749	2	S69972 Tyb protein - yeast	1.73e-01
21	110	6.2	411	2	C70343 conserved hypothetical	3.80e-01
22	110	6.2	433	2	T14282 embryonic callus pr	3.80e-01
23	108	6.1	225	2	C70422 hypothetical protein	6.39e-01

24	108	6.1	226	2	F64507 hypothetical protein	6.39e-01
25	105	6.0	868	2	T02635 D2 protein homolog -	1.38e+00
26	106	6.0	1328	2	S50948 Tyb protein - yeast	1.07e+00
27	106	6.0	1328	2	S52481 Tyb protein - yeast	1.07e+00
28	105	6.0	1328	2	B28097 Tyb protein - yeast	1.38e+00
29	106	6.0	1755	2	S69963 Tyb protein - yeast	1.07e+00
30	106	6.0	1755	2	S69960 Tyb protein - yeast	1.07e+00
31	106	6.0	1755	2	S69979 Tyb protein - yeast	1.07e+00
32	106	6.0	1755	2	S69866 Tyb protein - yeast	1.07e+00
33	106	6.0	1755	2	S69839 Tyb protein - yeast	1.07e+00
34	106	6.0	1755	2	S69980 Tyb protein - yeast	1.07e+00
35	106	6.0	1755	2	S50663 Tyb protein - yeast	1.07e+00
36	106	6.0	1755	2	S69955 Tyb protein - yeast	1.07e+00
37	106	6.0	1755	2	S70298 Tyb protein - yeast	1.07e+00
38	106	6.0	1755	2	S50641 Tyb protein YER138c	1.07e+00
39	106	6.0	1755	2	S69975 Tyb protein - yeast	1.07e+00
40	106	6.0	1755	2	S69982 Tyb protein - yeast	1.07e+00
41	106	6.0	1755	2	S57045 Tyb protein - yeast	1.07e+00
42	105	6.0	1755	2	S69957 Tyb protein - yeast	1.38e+00
43	106	6.0	1756	2	S69983 Tyb protein - yeast	1.07e+00
44	106	6.0	1793	2	S52601 Tyb protein - yeast	1.07e+00
45	106	6.0	1810	2	S69973 Tyb protein - yeast	1.07e+00

ALIGNMENTS

RESULT	ENTRY	TITLE	ORGANISM	DATE
1	ENSAB6	#type complete enterotoxin B precursor -	Staphylococcus aureus	
		#formal name Staphylococcus aureus		
		24-Apr-1984 #sequence revision 15-Oct-1996 #text change		
		18-Jun-1999		
ACCESSIONS	S27360; A92065; S27240; A01815			
REFERENCE	S27360			
#authors	Jones, C.L.; Khan, S.A.			
#journal	J. Bacteriol. (1986) 166:29-33			
#title	Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.			
#cross-references	MUID:86168029			
#accession	S27360			
#molecule_type	DNA			
#residues	1-266	#label JON		
#cross-references	EMBL:M1118; NID:g152999; PID:AAA8550.1;			
#accession	PID:g153000			
#experimental_source	strain S6			
REFERENCE	A92065			
#authors	Huang, I.Y.; Bergdoll, M.S.			
#journal	J. Biol. Chem. (1970) 245:3518-3525			
#title	The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.			
#cross-references	MUID:71007902			
#accession	A92065			
#molecule_type	protein			
#residues	28-55, 'NND', 59-68, 'NE', 71, 'FDLIV', 78-117, 119-127, 'N', 129, 'D', 131-152, 'ENT', 156-148, 'GN', 151-156, 'Y', 157-184, 'EQ', 187-232, 'N', 234-245, 'ND', 248-266	#label HVA		
#experimental_source	strain S-6			
REFERENCE	A92064			
#authors	Huang, I.Y.; Bergdoll, M.S.			
#journal	J. Biol. Chem. (1970) 245:3511-3517			
#title	The primary structure of staphylococcal enterotoxin B. II. Isolation, composition, and sequence of chymotryptic peptides.			
#cross-references	MUID:71007901			
#contents	annotation; chymotryptic peptides			
REFERENCE	A92063			
#authors	Huang, I.Y.; Bergdoll, M.S.			
#journal	J. Biol. Chem. (1970) 245:3493-3510			
#title	The primary structure of staphylococcal enterotoxin B. I. Isolation, composition, and sequence of tryptic peptides from oxidized enterotoxin B.			

```
#cross-references MUID:71007900
#contents      annotation: tryptic peptides
REFERENCE      A90548
#authors       Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.;
#journal       Dunnehy, D.A.; Bergdoll, M.S.
#title         Biochemistry (1965) 4:1011-1016
#cross-references MUID:66035792
#contents      annotation: biological source of protein
REFERENCE      S27240
#authors       Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.;
#journal       Moskaleva, E.Y.; Sveshnikov, P.G.; Pozdnyakova, L.P.;
#title         Eur. J. Biochem. (1992) 209:823-828
#cross-references MUID:93049338
#cross-references MUID:93049338
#accession     S27240
#molecule_type protein
#residues      28-42;128-148 #label ALA
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS        enterotoxin; extracellular protein; toxin
FEATURE         1-27
#domain signal sequence #status predicted #label SIG\
28-266          #product enterotoxin B #status experimental
120-140          #disulfide_bonds #status experimental
SUMMARY         #length 266 #molecular-weight 31436 #checksum 4249

Query Match      99.8%; Score 1760; DB 1; Length 266;
Best Local Similarity 99.6%; Pred. No. 2,96e-284;
Matches 238; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 28 ESOPDPKPEDELHKSSKFTGLMENNKKVLYDDNHVSAIIVKSIDOFLYDLISIKDTLGN 87
QY 1 ESOPDPKPEDELHKSSKFTGLMENNKKVLYDDNHVSAIIVKSIDOFLYDLISIKDTLGN 60
88 YDNVRYEFKKNDLADKKYKDYVDFGANYYYOCYFSKRTKDINSHTDKRKTMYGGVTE 147
61 YDNVRYEFKKNDLADKKYKDYVDFGANYYYOCYFSKRTKDINSHTDKRKTMYGGVTE 120
Db 148 HNGNQLDKYKSTYRVEDGKNLISFDVQTNKKKVTYAOELDYLTRHYLVKNNKLYEFNNS 207
QY 121 HNGNQLDKYKSTYRVEDGKNLISFDVQTNKKKVTYAOELDYLTRHYLVKNNKLYEFNNS 180
Db 208 PYENGVIKFTIENENKSFYDMMAPAGDKFDOSKYLMMYNDKMKVDSKVTEVYLTTRKK 266
QY 181 PYENGVIKFTIENENKSFYDMMAPAGDKFDOSKYLMMYNDKMKVDSKVTEVYLTTRKK 239

RESULT 2
ENTRY      ENSAC1 #type complete
TITLE      enterotoxin C-1 precursor - Staphylococcus aureus
ORGANISM   #formal_name Staphylococcus aureus
DATE       15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change
18-Jun-1999
ACCESSIONS S06356; A01816
REFERENCE    S06356
#authors     Bohach, G.A.; Schlievert, P.M.
#journal     Mol. Gen. Genet. (1987) 209:15-20
#title       Nucleotide sequence of the staphylococcal enterotoxin C1 gene
#cross-references MUID:88038352
#accession   S06356
#molecule_type DNA
#residues    1-266 #label BOH
#cross-references EMBL:X05815; NID:946566; PIDN:CAA29260.1; PID:946567
REFERENCE     A01816
#authors     Schmidt, J.J.; Spero, L.
#journal     J. Biol. Chem. (1983) 258:6300-6306
#title       The complete amino acid sequence of Staphylococcal
#cross-references MUID:83213327
#accession   A01816
```

```
#molecule_type protein
#residues      28-75,'IL','78-176,'N',178-266 #label SCH
GENETICS
CLASSIFICATION #gene      entC1
#superfamily enterotoxin B
KEYWORDS        enterotoxin
FEATURE         1-27
#domain signal sequence #status predicted #label SIG\
28-266          #product enterotoxin C-1 #status experimental #label
#accession     MUI\
120-137         #disulfide_bonds #status experimental
SUMMARY         #length 266 #molecular-weight 30546 #checksum 4489

Query Match      67.1%; Score 1183; DB 1; Length 266;
Best Local Similarity 66.8%; Pred. No. 1.19e-180;
Matches 161; Conservative 40; Mismatches 34; Indels 6; Gaps 6;

Db 28 ESOPDPKPEDELHKSSKFTGLMENNKKVLYDDHYVSATRVKSVDFLAHDLIYNISDKKLKN 87
QY 1 ESOPDPKPEDELHKSSKFTGLMENNKKVLYDDNHVSAIIVKSIDOFLYDLISIKDTLGN 60
88 YDKVKTFLDLNGLAKKTKDEYVDYGSNYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 144
QY 61 YDNVRYEFKKNDLADKKYKDYVDFGANYYYOCYFSKRTKDINSHTDKRKTMYGGVTE 120
145 HEGNHFPNGNLQNVLYVYENKRTISFEVOTDKKSYTAOELDIKARNFLINKKNLYEFN 204
QY 121 HNGNQLDK-Y-RSITTVYFEDGKNLISFDVQTNKKKVTYAOELDYLTRHYLVKNNKLYEFN 178
Db 205 SSPETGYIKFTIENNGTFFWYDMMAPAGDKFDOSKYLMMYNDKMKVDSKVTEVYLTTRK 264
QY 179 NSPETGYIKFTIENE-NSFWYDMMAPAGDKFDOSKYLMMYNDKMKVDSKVTEVYLTTRK 237
Db 265 N 265
QY 238 K 238

RESULT 3
ENTRY      S11885 #type complete
TITLE      enterotoxin C3 - Staphylococcus aureus
ORGANISM   #formal_name Staphylococcus aureus
DATE       19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
16-Jul-1999
ACCESSIONS S11885
REFERENCE    S11885
#authors     Hovde, C.J.; Hackett, S.P.; Bohach, G.A.
#journal     Mol. Gen. Genet. (1990) 220:329-333
#title       Nucleotide sequence of the staphylococcal enterotoxin C3
#cross-references MUID:90220508
#accession   S11885
#molecule_type DNA
#residues    1-266 #label HOV
#cross-references CB:X51661; NID:946570; PIDN:CAA35972.1; PID:946571
CLASSIFICATION #superfamily enterotoxin B
SUMMARY       #length 266 #molecular-weight 30671 #checksum 6135

Query Match      65.6%; Score 1156; DB 2; Length 266;
Best Local Similarity 66.0%; Pred. No. 7.73e-176;
Matches 159; Conservative 40; Mismatches 36; Indels 6; Gaps 6;

Db 28 ESOPDPKPEDELHKSSKFTGLMENNKKVLYDDHYVSATRVKSVDFLAHDLIYNISDKKLKN 87
QY 1 ESOPDPKPEDELHKSSKFTGLMENNKKVLYDDNHVSAIIVKSIDOFLYDLISIKDTLGN 60
88 YDKVKTFLDLNGLAKKTKDEYVDYGSNYVNCYFSSK-DNV-GKVTGG-KTCMYGGITK 144
QY 61 YDNVRYEFKKNDLADKKYKDYVDFGANYYYOCYFSKRTKDINSHTDKRKTMYGGVTE 120
145 HEGNHFPNGNLQNVLYVYENKRTISFEVOTDKKSYTAOELDIKARNFLINKKNLYEFN 204
```

121 HNGNLDK-Y-RSITVRFEEDGKNLSPDVOTNKKVTAQELDYTRITVLYKNNKLYEEN 178
179 NSPYETGIRKFIENE-NSFWYDMMPAPGDKFDQSKYLMYNDNKKVDSKDYIEVYLTTK 237
265 N 265
238 K 238

RESULT 4
ENTRY
TITLE A60114 #type complete
ALTERNATE_NAMES enterotoxin C-2 precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999

ACCESSIONS
REFERENCE A60114; B60114; A33866
#authors Bohach, G.A.; Schlievert, P.M.
#journal Infect. Immun. (1989) 57:2249-2252
#title Conservation of the biologically active portions of staphylococcal enterotoxins C1 and C2.
#cross-references MUID:89277549
#accession A60114
#status not compared with conceptual translation
#molecule_type DNA
#residues 1-266 ##label BOH
#accession B60114
#molecule_type protein
#residues 28-66 ##label BOH2

REFERENCE A33866
#authors Couch, J.L.; Betley, M.J.
#journal J. Bacteriol. (1989) 171:4507-4510
#title Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests that intergenic recombination causes antigenic variation.
#cross-references MUID:89327174
#accession A33866
#status preliminary
#molecule_type DNA
#residues 1-266 ##label COU
#cross-references GB:M28364; NID:9153003; PIDN:AAA26624.1; PID:9153004

GENETICS
#gene entC2
CLASSIFICATION #superfamily enterotoxin B
FEATURE 1-27 #domain signal sequence #status predicted #label SIG
28-266 #product enterotoxin C-2 #status predicted #label MAT
SUMMARY #length 266 #molecular_weight 30604 #checksum 5494

Query Match 65.1%; Score 1148; DB 2; Length 266;
Best Local Similarity 65.6%; Pred. No. 2.05e-174;
Matches 18; Conservative 40; Mismatches 37; Indels 6; Gaps 6;

Db 28 ESQDPPTDELLHKSSEFTGMMKMYLYDXDHYVSATKYMSVDKFLAHLIYNISDKILN 87
1 ESQDPKRDLEHKSSTFGMLMKVLYDXDNHVSAINKSIDOFLYRDLISIRKTKLGN 60
88 YDKVKTLLNEDLAKKYDEVVDVYGSNYVYCFSSK-DNV-GKVTGG-KTCMYGGITK 144
61 YDNVVEFKNKNDLADKYKDYVDVFGANYVYOCYFSKKTNDINSHTDCKRKTGMYGVTE 120
145 HEGNFDGNGNONTVIRYENKRNITISFENQTDKKSVAQELDIARFNLINKKLYEEN 204
121 HNGNLDK-Y-RSITVRFEEDGKNLSPDVOTNKKVTAQELDYTRITVLYKNNKLYEEN 178
205 NSPYETGIRKFIENGNFTWYDMMPAPGDKFDQSKYLMYNDNKTVDKSKVYIEVYLTTK 264
179 NSPYETGIRKFIENE-NSFWYDMMPAPGDKFDQSKYLMYNDNKKVDSKDYIEVYLTTK 237

Db 265 N 265
238 K 238

RESULT 5
ENTRY
TITLE S29659 #type complete
ALTERNATE_NAMES exotoxin type A precursor (allele 1) - Streptococcus pyogenes
ORGANISM #formal_name Streptococcus pyogenes phase T12
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

ACCESSIONS
REFERENCE S29659; S18782; S18784; S18785; S18791; S18796; S18797;
S18800
#authors Weeks, C.R.; Ferretti, J.J.
#journal Infect. Immun. (1986) 52:144-150
#title Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.
#cross-references MUID:86166804
#accession S29659
#molecule_type DNA
#residues 1-251 ##label WFE
#cross-references GB:U04053; EMBL:M19350; NID:91877426; PIDN:AAC48868.1; PID:91877430

REFERENCE S18782
#authors Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal J. Exp. Med. (1991) 174:1271-1274
#title Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession S18782
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 9-244 ##label NEL
#cross-references EMBL:X61560; NID:947287; PIDN:CAA43758.1; PID:947288
#experimental_source Streptococcus pyogenes strain MGA5165 isolate Nebraska unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18784
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 9-244 ##label NEA
#cross-references EMBL:X61556; NID:947291; PIDN:CAA43754.1; PID:947292
#experimental_source Streptococcus pyogenes strain MGA5167 isolate Minnesota unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18785
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 9-244 ##label NEZ
#cross-references EMBL:X61559; NID:947293; PIDN:CAA43757.1; PID:947294
#experimental_source Streptococcus pyogenes strain MGA5167 isolate Texas unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18791
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 9-244 ##label NEY
#cross-references EMBL:X61555; NID:947309; PIDN:CAA43753.1; PID:947310
#experimental_source Streptococcus pyogenes strain MGA5327 isolate Arizona unassigned phage
#note the nucleotide sequence was submitted to the EMBL Data Library, September 1991

#accession S18796
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA

```

##residues      9-244 ##label NEO
##cross-references EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:g47320
##experimental_source Streptococcus pyogenes strain MGAS493 isolate
#note          the nucleotide sequence was submitted to the EMBL Data
               Library, September 1991

#accession     S18797
##status       nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues     9-244 ##label NEH
##cross-references EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:g47322
##experimental_source Streptococcus pyogenes strain MGAS494 isolate
#note          France unassigned phage
               the nucleotide sequence was submitted to the EMBL Data
               Library, September 1991

#accession     S18800
##status       nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues     9-228 ##label NES
##cross-references EMBL:X61554; NID:g47327; PIDN:CAA43752.1; PID:g47328
##experimental_source Streptococcus pyogenes strain MGAS500 isolate New
               Zealand unassigned phage
               the nucleotide sequence was submitted to the EMBL Data
               Library, September 1991

GENETICS
#gene          speA: speA1
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS       exotoxin
FEATURE        1-30   #domain signal sequence #status predicted #label SIG\
                  product exotoxin type A #status predicted #label MAT
SUMMARY        1-251  #length 251 #molecular-weight 29246 #checksum 1475

Query Match    42.3%; Score 746; DB 1; Length 251;
Best Local Similarity 50.2%; Pred. No. 1,75e-103;
Matches 119; Conservative 43; Mismatches 59; Indels 16; Gaps 9;

Db            30 AOODPNSQLHRSSLVKWL-QNIYFLYEGDPVTHENKVSVDQLSHDLINVGSP--NY 85
              :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy           2 SQDPPKPDELHKSSFGLTGMENMKVLYDDNHSAINVKSIDQFLYFLDIYSIKPTKLGN 61
              ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db            86 DKLTKELKNQEMATLEFKKNNDIVGEVEYYHCYLCLC---E-NA-E---RSACITGCVTNH 136
              |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy           62 DNVRVEFNKKADLDKRYKYDVFGANYYOCYFSKKTNDINSHEHTDKRKTCMGVTEH 121
              ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db            137 EGNHLIEPKILVKVYSIDGISLSEDIETNKKNWTAQELDVKYKRLTDNQLTYNPSK 196
              ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy           122 NGNQLDKYSTIVRPFEDCKNLISPDVOTNNKKVTYAQELDVLTRHYLVKKKKILEFPNNSP 181
              ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db            197 YETGYIKIFPKNKESFDFPEEP-E-FYOSKTYIMTYKDNFTLDSNTSOLEYVITTK 251
              |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy           182 YETGYIKIFI-ENENSFWMDMPAPGDCKFDQSKYLMYNDNMKVSDVKIEVYLTTK 237
              |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT        6
ENTRY         S18789 #type fragment
TITLE         exotoxin A precursor (allele 4) - Streptococcus pyogenes
              (strain MGAS262 isolate California) (fragment)
ALTERNATE_NAMES scarlet fever toxin
ORGANISM      #formal name Streptococcus pyogenes
VARIETY       strain MGAS262 isolate California
DATE          29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
              16-Jul-1999

ACCESSIONS   S18789
REFERENCE     S18782
#authors      Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal      J. Exp. Med. (1991) 174:1271-1274
#title        Characterization and clonal distribution of four alleles of
              the speA gene encoding pyrogenic exotoxin A (scarlet fever
              toxin) in Streptococcus pyogenes.
#cross-references MUID:92044323
#accession    S18789
#status       nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues     1-236 ##label NEA
#cross-references EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
#experimental_source strain MGAS485 isolate Yugoslavia unassigned phage
#note          the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991

nucleic acid sequence not shown; translation not shown

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accessions	S18794	status	nucleic acid sequence not shown; translation not shown						
##status		##molecule_type	DNA						
##residues	1-236	##label	NEZ						
##cross-references	EMBL:X61570; NID:947315; PIDN:CAA43768.1; PID:947316	##experimental_source	strain MGAS491 isolate United Kingdom unassigned phage						
##note	the nucleotide sequence was submitted to the EMBL Data Library, September 1991								
##accession	S18801	status	nucleic acid sequence not shown; translation not shown						
##status		##molecule_type	DNA						
##residues	1-236	##label	NEV						
##cross-references	EMBL:X61572; NID:947333; PIDN:CAA43770.1; PID:947334	##experimental_source	strain MGAS624 isolate Germany unassigned phage						
##note	the nucleotide sequence was submitted to the EMBL Data Library, September 1991								
##accession	S18798	status	nucleic acid sequence not shown; translation not shown						
##status		##molecule_type	DNA						
##residues	1-236	##label	NEO						
##cross-references	EMBL:X61571; NID:947323; PIDN:CAA43769.1; PID:947324	##experimental_source	strain MGAS495 isolate Germany unassigned phage						
##note	the nucleotide sequence was submitted to the EMBL Data Library, September 1991								
GENETICS		spea3							
##gene	CLASSIFICATION	##superfamily	enterotoxin B						
KEYWORDS		exotoxin							
FEATURE	1-22	##domain	signal sequence (fragment) #status predicted						
		##label	Stg\						
23-236		##product	exotoxin type A (fragment) #status predicted						
		##label	MAT						
SUMMARY	##length	236	##checksum	612					
Query Match	39.48;	Score	694;	DB.2;	Length	236;			
Best Local Similarity	48.35;	Pred. No.	1.92e-94;						
Matches	111;	Conservative	44;	Mismatches	59;	Indels	16;	Gaps	9;
Db	22	AADPDPQSALHRSRLVKNL-QNITFLYEGDPVYHENVKSVOLDLSHDLTYNVSQP---NY	77						
QY	2	SQPPKRFDELHKKSKFLGEMKNKVLDDNHNVAIWKSIDQFLFYDLTYSIKDKLGNV	61						
Db	78	DKLTETLKNQEMATLFPKKNIDIVGYEYHLCYLCL---E-NA-E---RSACIYGVTNH	128						
QY	62	DNVAVEERKNMDLADKYDKYVDVFGANYTYQCCEFSKKTNDINSHEDRKRTCMGCVTEH	121						
Db	129	EGNHLETPKRIIVKVSIDGQSIFDIETNKKKAVTVAQELDYKVRKYLTDNKKOLYTNPSK	188						
QY	122	NGNOLDYRSITVAVEFDGKNLLSPFVQTKKKVTAQOELDYLTRHLYNKKRLYEFNNSP	181						
Db	189	YETGYIKFIPKKNESFWEDEFPPR-E-FIOSKTLMIYKNDENTLDSSTSI	236						
QY	182	YETGYIKFL-ENENSEFWYDMMPAPGDKFDQSKYLMYINDKNKVDSDVKI	230						
RESULT	8								
ENTRY	S18786	##type	fragment						
TITLE	exotoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isolate California and others) (fragment)								
ALTERNATE_NAMES	scarlet fever toxin								
ORGANISM	#formal name Streptococcus pyogenes phage								
##variety	strain MGAS250 isolate California; strain MGAS251 isolate California; strain MGAS256 isolate California; strain MGAS285 isolate Colorado; strain MGAS480 isolate Yugoslavia; strain MGAS492 isolate United Kingdom; strain MGAS496 isolate Germany								
DATE	29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999								
ACCESSIONS	S18786; S18787; S18788; S18790; S18792; S18795; S18799								
REFERENCE	S18782								

```

#authors      Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
#journal      J. Exp. Med. (1991) 174:1271-1274
#title        Characterization and clonal distribution of four alleles of
              the spa gene encoding pyrogenic exotoxin A (scarlet fever
              toxin) in Streptococcus pyogenes.
#cross-references MIM:92044323
#accession   S18786
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:g47297; PIDN:CAA43759.1; PID:g47298
##experimental_source strain MGA5250 isolate California unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18787
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:g47299; PIDN:CAA43760.1; PID:g47300
##experimental_source strain MGA5251 isolate California unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18788
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:g47301; PIDN:CAA43761.1; PID:g47302
##experimental_source strain MGA5256 isolate California unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18790
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:g47305; PIDN:CAA43762.1; PID:g47306
##experimental_source strain MGA5285 isolate Colorado unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18792
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:g47311; PIDN:CAA43763.1; PID:g47312
##experimental_source strain MGA5480 isolate Yugoslavia unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18795
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61561; NID:g47317; PIDN:CAA43764.1; PID:g47318
##experimental_source strain MGA5492 isolate United Kingdom unassigned
              phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
#accession   S18799
##status      nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues    1-236 ##label NEI
##cross-references EMBL:X61567; NID:g47325; PIDN:CAA43765.1; PID:g47326
##experimental_source strain MGA5496 isolate Germany unassigned phage
##note        the nucleotide sequence was submitted to the EMBL Data
              Library, September 1991
GENETICS
#gene         spa2
CLASSIFICATION #superfamily enterotoxin B
KEYWORDS      exotoxin
FEATURE
1-22
23-236
#domain signal sequence (fragment) #status predicted
#label STG\
#product exotoxin type A (fragment) #status predicted
#label MT
#length 236 #checksum 1685
SUMMARY

```

Query Match 39.1%; Score 690; DB 2; Length 236;
Best Local Similarity 48.3%; Pred. No. 9,49e-94;
Matches 111; Conservative 44; Mismatches 59; Indels 16; Gaps 9;

Db 22 AOODPDSQSLHRRSLVKNL-QNIFYLEGDPVTHENKSVQDLSDHLDIYNVSGP---NY 77
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 78 DKJKTLEKNDEMTLFDKNDVIYSEYHLCYLC---E-NA-E---RSACLYGVTNH 128
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 129 EGNHLEIPKRIYVVSIDGLOSFDIETNKKMTVAQELDYKRVYLTDNKQLYTNGPSK 188
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 122 NGNOLDKRSITRYKVFEDGKNLSFDVQTKKKYTAQELDLYTHRYLVKNNKLYEFNNSP 181
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 189 YETGYIKFI-PKNESEFWDFEPEP-E-FTQSKYLMYIKDNETLDSNTSQI 236
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 182 YETGYIKFI-ENESFWYDMMPAPGDKFDQSKYLMYNDNMKNDKVDVKI 230
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

RESULT 9
ENTRY A26152 #type complete
TITLE streptococcal pyrogenic exotoxin type A precursor -
ALTERNATE_NAMES scarlet fever toxin; SPE type A (speak)
ORGANISM #formal_name Streptococcus sp.
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

ACCESSIONS A26152
REFERENCE A26152
#authors Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
#journal Mol. Gen. Genet. (1986) 203:354-356
#title Streptococcal pyrogenic exotoxin type A (scarlet fever toxin)
#cross-references M18970; NID:g153120; PID:g153121
#accession A26152
#molecule-type DNA

CLASSIFICATION #superfamily enterotoxin B
KEYWORDS exotoxin
SUMMARY #length 250 #molecular-weight 29168 #checksum 8233

Query Match 33.9%; Score 598; DB 1; Length 250;
Best Local Similarity 43.8%; Pred. No. 7,07e-78;
Matches 102; Conservative 47; Mismatches 67; Indels 17; Gaps 10;

Db 34 PKPSQLOSRNLVYTFKIFYEFM-RVTLVTHBNKSVQDLSDHLDIYNVSGP---NYDKL 89
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
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#superfamily enterotoxin B

Db 6 PKDELHKSSEKFGMLNKMVLVDNHNVSAINVKSIDQFLFDLYSIRKTKLGNTDNR 65
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 90 TELKNDEMTLFDKNDVIYSEYHLCYLC---E-NA-E---RSACLYGVTNH 140
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
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#status preliminary
#residues 1-250 ##label JOH
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#superfamily enterotoxin B

Db 66 VEFKNKDLADKYDKYDVGVANYYQCYFSKKTNDINSHETDKRRTCMGVTEHNGQ 125
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
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#status preliminary
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##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 141 LEIPKRIYVVSIDGLOSFDIETNKKMTVAQELDYKRVYLTDNKQLYTNGPSK 199
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
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#status preliminary
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##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 126 LDKYRSITRYKVFEDGKNLSFDVQTKKKYTAQELDLYTHRYLVKNNKLYEFNNSP 185
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
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#molecule-type DNA
#status preliminary
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#superfamily enterotoxin B

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#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
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#accession A33953
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#status preliminary
#residues 1-250 ##label JOH
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#superfamily enterotoxin B

Db 186 YKIFIPKNESEFWDFEPEP-E-FTQSKYLMYIKDNETLDSNTSQI 237
#journal J. Bacteriol. (1989) 171:479-4806
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#accession A33953
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##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

RESULT 10
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TITLE enterotoxin D precursor - Staphylococcus aureus
ORGANISM #formal_name Staphylococcus aureus
DATE 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 26-Aug-1999
ACCESSIONS A33953
REFERENCE A33953

#authors Bayles, K.W.; Iandolo, J.J.
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
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#status preliminary
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#superfamily enterotoxin B

Db 33 KEKELHKSSEKFGMLNKMVLVDNHNVSAINVKSIDQFLFDLYSIRKTKLGNTDNR 65
#journal J. Bacteriol. (1989) 171:479-4806
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#accession A33953
#molecule-type DNA
#status preliminary
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#superfamily enterotoxin B

Db 7 KPDELHKSSEKFGMLNKMVLVDNHNVSAINVKSIDQFLFDLYSIRKTKLGNTDNR 64
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
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#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 93 LIPNFKEMAOHFKSKVNDVYPIRYSINCY-G---GEI-----D-RACIYGVTHREGN 142
#journal J. Bacteriol. (1989) 171:479-4806
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#accession A33953
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#superfamily enterotoxin B

Db 65 RVEFKNKDLADKYDKYDVGVANYYQCYFSKKTNDINSHETDKRRTCMGVTEHNGQ 124
#journal J. Bacteriol. (1989) 171:479-4806
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#accession A33953
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#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 143 KLKERRKIPINLMINGVQKESLDKVDYDKNVTYQELDQARRYLQDKLYNNDTLGG 202
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
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#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 125 QLDKYSITRYKVFEDGKNLSFDVQTKKKYTAQELDLYTHRYLVKNNKLYEFNNSP 181
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
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#accession A33953
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#status preliminary
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#superfamily enterotoxin B

Db 203 KIORGKIEPDSQSKVSYDLFDVKG-D-FPE-KQLRIYSQNTKLTSTHLDIYLYEK 258
#journal J. Bacteriol. (1989) 171:479-4806
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#status preliminary
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#superfamily enterotoxin B

Db 182 -YETGYIKFI-ENESFWYDMMPAPGDKFDQSKYLMYNDNMKNDKVDVKI 237
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#status preliminary
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#superfamily enterotoxin B

RESULT 11
ENTRY A28664 #type complete
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FRI337)
ORGANISM #formal_name Staphylococcus aureus
DATE 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 26-Aug-1999

ACCESSIONS A28664
REFERENCE A28664
#authors Betley, M.J.; Mekalanos, J.J.
#journal J. Bacteriol. (1988) 170:34-41
#title Nucleotide sequence of the type A staphylococcal enterotoxin
#cross-references M18970; NID:g153120; PID:g153121
#accession A28664
#molecule-type DNA

CLASSIFICATION #superfamily enterotoxin B
KEYWORDS enterotoxin
SUMMARY #length 257 #molecular-weight 29669 #checksum 2543

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Best Local Similarity 35.0%; Pred. No. 2,27e-40;
Matches 82; Conservative 56; Mismatches 77; Indels 19; Gaps 12;

Db 35 DLKRSQLOSTALGNLKOIYVNEKATKNEKSHDOFLQHTILFKGFFTDHSWYNLDLD 94
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 10 ELKRSKFTGL-MENK-VLYDNHNVSAINVKSIDQFLFDLYSIRKTKLGNTDNR 67
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 95 FDSKDIYDKYKGRKVDLYGAYGYQC---AGC--T--PNK-TACMYGCVTLHDNNRLT 144
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 68 FKNKDLADKYDKYDVGVANYYQCYFSKKTNDINSHETDKRRTCMGVTEHNGQ 127
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 145 EEKVPINLMDGKONTVPLETYKTKKNTYQELDQARRYLQDKLYNNDTLGG 204
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 128 KYSITRYKVFEDGKNLSFDVQTKKKYTAQELDLYTHRYLVKNNKLYEFNNSP 183
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Db 205 RGLIVFTSTPEPVNVDLFGAQQG-YSENT-LRLRYDNKTIENSENHIDLYLT 256
#journal J. Bacteriol. (1989) 171:479-4806
#title Genetic and molecular analyses of the gene encoding
#cross-references M18970; NID:g153120; PID:g153121
#accession A33953
#molecule-type DNA
#status preliminary
#residues 1-250 ##label JOH
##cross-references GB:M18970; NID:g153120; PID:g153121
#superfamily enterotoxin B

Qy	184	TYGIKF-IENENSPFYDMMPAPGDKFDQSKSYLLMAYNDNMKNVDSKVKEIVLYLT	236	
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ENTRY	A29566	#type complete		
TITLE	enterotoxin A - Staphylococcus aureus			
ORGANISM	#formal_name Staphylococcus aureus			
DATE	05-Jun-1988	#sequence_revision 05-Jun-1988	#text_change 18-Jun-1993	
ACCESSIONS	A29566			
REFERENCE	A29566			
#authors	Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.			
#journal	J. Biol. Chem. (1987) 262:7006-7013			
#title	Complete amino acid sequence of staphylococcal enterotoxin A			
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Db	11	DLRKSELGALGNLKOIYYNEKATEKESHDQFLQHTILFKGFPHDSWYDLDVLD	70	
Qy	10	ELHKSFKFTGL-MENKM-VLYDNNHVSAINVKSIDQFLYFDLISIKDKRLGNYDNVRYE	67	
Db	71	FDSKDIDYDKYKKVVDLYGAYVYGQ----AGG--T--PNK-TAGMGVGLHNNRLT	120	
Qy	68	FKMKDLADKIDKVDYDFGANYTYOQCFSKKIDINDSHETDKKTKTCMGVTEHNGNOLD	127	
Db	121	EEKRVPIMLMDGQNTVPLETVKTNKNTVOELDLQARRYLQEKYKNLYNSDVFEGKVQ	180	
Qy	128	KYRSITVRVFEDEK-NLISFD-VQTNKKKTYAQELDYLFRLHYLVKKKILYEN--NSPYE	183	
Db	181	RGILVFHTSTEPSVNYDLFGAQGQ-YSN-T-LRLIYRDNKSINSENMHDIYLYT	232	
Qy	184	TYGIKF-IENENSPFYDMMPAPGDKFDQSKSYLLMAYNDNMKNVDSKVKEIVLYLT	236	
RESULT	13			
ENTRY	A28179	#type complete		
TITLE	enterotoxin E precursor - Staphylococcus aureus			
ORGANISM	#formal_name Staphylococcus aureus			
DATE	30-Jun-1989	#sequence_revision 30-Jun-1989	#text_change 26-Aug-1999	
ACCESSIONS	A28179			
REFERENCE	A28179			
#authors	Couch, J.L.; Solits, M.T.; Betley, M.J.			
#journal	J. Bacteriol. (1988) 170:2954-2960			
#title	Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.			
#cross-references	MUDD:88257005			
#accession	A28179			
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Db	95	UGSDADNKKKKGVLDVLYGAYVCQ----	-AGC--T--PNK--TTCMGCVTLHNNRJT	144
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Oy	128	KYRSITVRVPEDEKNL-LSPD-VQTNKKKVTAGLELDYLRHLYLVNKKLKYEFNN-SP-YE	183	
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Oy	184	TGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDKNMVDSDVKYKIEVYLT	236	
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DATE		31-Dec-1998	#sequence_revision 31-Dec-1988	#text_change
ACCESSIONS		A30509		
REFERENCE		Goshorn, S.C.; Schlievert, P.M.		
#authors		Infect. Immun. (1988) 56:2518-2520		
#journal		Nucleotide sequence of streptococcal pyrogenic exotoxin type C		
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			Indels 6;	Gaps 6;
Db	113	TYGTTTPAQNKKV-NHLLGNLFPSGSOONLNKKIILEKDYTOEIDPFKTRKLYMDNY	171	
Oy	114	MYGGVTEHNGQDLKRYSI-TVRFEDGKNLLSFVDQTNKKVTAGLELDYLRHLYLVNKK	172	
Db	172	KIIV-ATSPYVSGIEIGTKDKGHEQDLEDSNEG-TSDFPAKKDNRRIINMKNFHF	229	
Oy	173	KLYEKNNSPYETGYIKFIENENSF-WYDMMPAPGDKFDQSKYLMYNDKNMVDSDK-VKI	230	
Db	230	DIYL 233		
Oy	231	EYVL 234		
RESULT	15			
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TITLE		probable Rheske (2Pe-2S) Iron-sulfur protein ynfW - Bacillus subtilis		
ORGANISM		#format_name Bacillus subtilis		
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REFERENCE		A69580		
#authors		Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloul, G.; Azevedo, V.; Bertolo, M.G.; Bessieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans, A.; Braun, M.; Bricnell, S.C.; Bron, S.; Brouillet, S.; Bruschli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codan, J.J.; Conerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emerson, P.T.; Ettian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Galleron, N.; Ghim, S.Y.; Glaser, P.; Goffeau, A.; Goldightly, E.J.; Grandi, G.; Giessepi, G.; Guy, B.J.; Haga, K.; Haehele, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hollio, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;		

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CLASSIFICATION
KEYWORDS
FEATURE
453-499
463,465,481,484
SUMMARY
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Best local Similarity
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Conservative
24;
Mismatch
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Gaps
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GGVTE-HNGQDLKRYRSTRVREDEKRLNLSFDVQTRKKRYTAO-ELDY--LTRHYLVKN
ARY-TEAANOALDIYKGIADH
KLTLEFNNSPYETGYIKETIENEN
6.6%; Score 117; DB 2; Length 509;
28.9%; Pred. No. 5,91e-02;
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Job time : 147 secs.
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DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DE ENTEROTOXIN TYPE C (SECOVINE) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria: Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13379; AAA26623.1; -.
DR HSSP: P34071; 1SE2.
DR PFAM: PF01123; Staph_Scrt-toxin; 1.
DR Enterotoxin; Toxin; Superantigen.
FT NON TER 1
SO SEQUENCE 239 AA; 27517 MW; 1293E9CA CRC32;

Query Match 66.3%; Score 1169; DB 2; Length 239;
Best Local Similarity 66.8%; Pred. No. 2.24e-193;
Matches 161; Conservative 38; Mismatches 36; Indels 6; Gaps 6;

DB 1 ESOPDPDPDLHRSKSTGTGLMNNKLYLDHYVATKVSVDKFLADLYNITSDDKLTN 60
OY 1 ESOPDPDPDLHRSKSTGTGLMNNKLYLDHYVATKVSVDKFLADLYNITSDDKLTN 60
DB 61 YDKVKTLELNLAKKXKDEVDYVGSNYVNCYFSSK-DNV-GKVTG-KTCMYGKITR 117
OY 61 YDKVKTLELNLAKKXKDEVDYVGSNYVNCYFSSK-DNV-GKVTG-KTCMYGKITR 117
DB 61 YDNVRFVFKKDLADKKYDVFAGANYVYOCFSSKKTNDINSHEDKRTKTCMYGVT 120
OY 61 YDNVRFVFKKDLADKKYDVFAGANYVYOCFSSKKTNDINSHEDKRTKTCMYGVT 120
DB 118 HEGNHDPGNLQNVLYRVYENKRTISFEVQTDKSVTAOELDIKARSLINKNLYEFN 177
OY 118 HEGNHDPGNLQNVLYRVYENKRTISFEVQTDKSVTAOELDIKARSLINKNLYEFN 177
DB 121 HNGNQLDK-Y-RSTIVRVFEDGKNLISFDVQTNKKVTAOELDYLTRHYLVKKNKLYEFN 178
OY 121 HNGNQLDK-Y-RSTIVRVFEDGKNLISFDVQTNKKVTAOELDYLTRHYLVKKNKLYEFN 178
DB 178 SSPYETGYIKFIENNGTFYVDMMPAPGDKFDSKYLMTYNDNKNMDSKDVKTEVYLTTR 237
OY 178 SSPYETGYIKFIENNGTFYVDMMPAPGDKFDSKYLMTYNDNKNMDSKDVKTEVYLTTR 237
DB 238 N 238
OY 238 K 238

RESULT 3
ID 006532 PRELIMINARY: PRT: 239 AA.
AC 006532;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DE ENTEROTOXIN TYPE C-7 (SEC740N) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria: Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-740N;

RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13375; AAA26619.1; -.
DR HSSP: P34071; 1SE2.
DR PFAM: PF01123; Staph_Scrt-toxin; 1.
DR Enterotoxin; Toxin; Superantigen.
FT NON TER 1
SO SEQUENCE 239 AA; 27642 MW; 81CA4BC2 CRC32;

Query Match 65.9%; Score 1162; DB 2; Length 239;
Best Local Similarity 66.0%; Pred. No. 5.02e-192;
Matches 159; Conservative 41; Mismatches 35; Indels 6; Gaps 6;

DB 1 ESOPDPDPDLHRSSEFTGTMDNKKLYLDHYVATKVSVDKFLADLYNITSDDKLTN 60
OY 1 ESOPDPDPDLHRSSEFTGTMDNKKLYLDHYVATKVSVDKFLADLYNITSDDKLTN 60
DB 61 YDKVKTLELNLAKKXKDEVDYVGSNYVNCYFSSK-DNV-GKVTG-KTCMYGKITR 117
OY 61 YDKVKTLELNLAKKXKDEVDYVGSNYVNCYFSSK-DNV-GKVTG-KTCMYGKITR 117
DB 61 YDNVRFVFKKDLADKKYDVFAGANYVYOCFSSKKTNDINSHEDKRTKTCMYGVT 120
OY 61 YDNVRFVFKKDLADKKYDVFAGANYVYOCFSSKKTNDINSHEDKRTKTCMYGVT 120
DB 118 HEGNHDPGNLQNVLYRVYENKRTISFEVQTDKSVTAOELDIKARSLINKNLYEFN 177
OY 118 HEGNHDPGNLQNVLYRVYENKRTISFEVQTDKSVTAOELDIKARSLINKNLYEFN 177
DB 121 HNGNQLDK-Y-RSTIVRVFEDGKNLISFDVQTNKKVTAOELDYLTRHYLVKKNKLYEFN 178
OY 121 HNGNQLDK-Y-RSTIVRVFEDGKNLISFDVQTNKKVTAOELDYLTRHYLVKKNKLYEFN 178
DB 178 SSPYETGYIKFIENNGTFYVDMMPAPGDKFDSKYLMTYNDNKNMDSKDVKTEVYLTTR 237
OY 178 SSPYETGYIKFIENE-NSFWYDMMPAPGDKFDSKYLMTYNDNKNMDSKDVKTEVYLTTR 237
DB 238 N 238
OY 238 K 238

RESULT 4
ID 006531 PRELIMINARY: PRT: 239 AA.
AC 006531;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DE ENTEROTOXIN TYPE C-4 (SEC4446) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria: Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-4446;
RX MEDLINE: 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL: L13374; AAA26618.1; -.
DR HSSP: P34071; 1SE2.
DR PFAM: PF01123; Staph_Scrt-toxin; 1.
DR Enterotoxin; Toxin; Superantigen.
FT NON TER 1
SO SEQUENCE 239 AA; 27612 MW; 52B18853 CRC32;

Query Match 65.4%; Score 1153; DB 2; Length 239;
Best Local Similarity 65.6%; Pred. No. 2.73e-190;
Matches 158; Conservative 41; Mismatches 36; Indels 6; Gaps 6;

Db 1 ESOPDMPDLDLHKSSEFTGTMGNMRYLYDDHYVATKYSVDFLAHDLIYNISDKLKN 60
1 ESOPDMPDLDLHKSSEFTGTMGNMRYLYDDHYVATKYSVDFLAHDLIYNISDKLKN 60
OY 1 ESOPDMPDLDLHKSSEFTGTMGNMRYLYDDHYVATKYSVDFLAHDLIYNISDKLKN 60
Db 61 YDKVTELLNEDLAKRYKDEVDVYGSNYVNCYFSSK-DNY-GKVTGS-KTCMYGATK 117
OY 61 YDKVTELLNEDLAKRYKDEVDVYGSNYVNCYFSSK-DNY-GKVTGS-KTCMYGATK 117
OY 61 YDNVAVEERKNMDLADKYDKDYDFGANYCYCFSKTNDINSHETDKRKTCTMGVATE 120
Db 118 HEGNHFDNGNLQNLVIRYENKRNITSEFVOTDKSVTAQELDIKARNFLLKKNLYEEN 177
OY 121 HNGNOLDK-Y-RSITVRYEEDGKNLISFDVOTNKKRYTAQELDYLTRHLYVKNKKLYEEN 178
Db 178 SSPYETGYIKFEIENNGNTFWYDMAPGDKFQSKYLLMYNDNKTVDKSKVIEVHLTK 237
OY 179 NSPIETGYIKFEIENE-NSFWYDMAPGDKFQSKYLLMYNDNKNVDSKDVIEVYLTTK 237
Db 238 N 238
OY 238 K 238

RESULT 5 PRELIMINARY; PRT: 239 AA.
ID 006533;
AC 006533;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE ENTEROTOXIN TYPE C (SECCOPELAND) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MNCOPELAND;
RX MEDLINE; 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL; L13378; AAA26622.1; -.
DR HSSP; P34071; 1STE.
DR PFAM; PF01123; Staph_toxin; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON-TER 1
SQ SEQUENCE 239 AA; 27651 MW; 7A5C4047 CRC32;

Query Match 65.2%; Score 1150; DB 2; Length 239;

Best Local Similarity 66.0%; Pred. No. 1,03e-189;
Matches 159; Conservative 39; Mismatches 37; Indels 6; Gaps 6;

Db 1 ESOPDMPDLDLHKSSEFTGTMGNMRYLYDDHYVATKYSVDFLAHDLIYNISDKLKN 60
OY 1 ESOPDMPDLDLHKSSEFTGTMGNMRYLYDDHYVATKYSVDFLAHDLIYNISDKLKN 60
Db 61 YDKVTELLNEDLAKRYKDEVDVYGSNYVNCYFSSK-DNY-GKVTGS-KTCMYGATK 117
OY 61 YDKVTELLNEDLAKRYKDEVDVYGSNYVNCYFSSK-DNY-GKVTGS-KTCMYGATK 117
OY 61 YDNVAVEERKNMDLADKYDKDYDFGANYCYCFSKTNDINSHETDKRKTCTMGVATE 120
Db 118 HEGNHFDNGNLQNLVIRYENKRNITSEFVOTDKSVTAQELDIKARNFLLKKNLYEEN 177
OY 121 HNGNOLDK-Y-RSITVRYEEDGKNLISFDVOTNKKRYTAQELDYLTRHLYVKNKKLYEEN 178
Db 178 SSPYETGYIKFEIENNGNTFWYDMAPGDKFQSKYLLMYNDNKTVDKSKVIEVHLTK 237
OY 179 NSPIETGYIKFEIENE-NSFWYDMAPGDKFQSKYLLMYNDNKNVDSKDVIEVYLTTK 237
Db 238 N 238

OY 238 K 238

RESULT 6 PRELIMINARY; PRT: 239 AA.
ID 006535;
AC 006535;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE ENTEROTOXIN TYPE C-3 (SEC3) (FRAGMENT).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRI 909;
RX MEDLINE; 94011313.
RA MARR J.C., LYON J.D., ROBERSON J.R., LUPHER M., BOHACH G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
PYROGENIC EXOTOXINS ARE ALL RELATED.
DR EMBL; L13377; AAA26621.1; -.
DR HSSP; P23133; 1JCK.
DR PFAM; PF01123; Staph_toxin; 1.
KW Enterotoxin; Toxin; Superantigen.
FT NON-TER 1
SQ SEQUENCE 239 AA; 27648 MW; 1DC80C35 CRC32;

Query Match 64.9%; Score 1145; DB 2; Length 239;

Best Local Similarity 64.3%; Pred. No. 9.52e-189;
Matches 155; Conservative 44; Mismatches 36; Indels 6; Gaps 6;

Db 1 ESOPDMPDLDLHKSSEFTGTMGNMRYLYDDHYVATKYSVDFLAHDLIYNISDKLKN 60
OY 1 ESOPDMPDLDLHKSSEFTGTMGNMRYLYDDHYVATKYSVDFLAHDLIYNISDKLKN 60
Db 61 YDKVTELLNEDLAKRYKDEVDVYGSNYVNCYFSSK-DNY-GKVTGS-KTCMYGATK 117
OY 61 YDKVTELLNEDLAKRYKDEVDVYGSNYVNCYFSSK-DNY-GKVTGS-KTCMYGATK 117
OY 61 YDNVAVEERKNMDLADKYDKDYDFGANYCYCFSKTNDINSHETDKRKTCTMGVATE 120
Db 118 HEGNHFDNGNLQNLVIRYENKRNITSEFVOTDKSVTAQELDIKARNFLLKKNLYEEN 177
OY 121 HNGNOLDK-Y-RSITVRYEEDGKNLISFDVOTNKKRYTAQELDYLTRHLYVKNKKLYEEN 178
Db 178 SSPYETGYIKFEIENNGNTFWYDMAPGDKFQSKYLLMYNDNKTVDKSKVIEVHLTK 237
OY 179 NSPIETGYIKFEIENE-NSFWYDMAPGDKFQSKYLLMYNDNKNVDSKDVIEVYLTTK 237
Db 238 N 238
OY 238 K 238
RESULT 7 PRELIMINARY; PRT: 239 AA.
ID 005157;
AC 005157;
DT 01-JUL-1997 (Tremblrel. 04, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TYPE C ENTEROTOXIN (FRAGMENT).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Bacillus/Staphylococcus group; Staphylococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-95-011195;
RA EDWARDS V.M., DERINGER J.R., CALANTINE S.D., DEOBALD C.F.,
RA BERGER P.H., KAPUR V., STAUFACHER C.V., BOHACH G.A.;
Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.

OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS 1842;
RX MEDLINE; 94222556.
RA REDA K.B., KAPUR V., MOLLICK J.A., LAMPEHEAR J.G., MUSSER J.M.,
RA RICH R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN-MGAS 1842;
RC MEDLINE; 96178602.
RX REDA K.B., KAPUR V., GOELA D., LAMPEHEAR J.G., MUSSER J.M., R.R.;
RA "Phylogenetic distribution of streptococcal superantigen ssa within
RT variants provides evidence for horizontal transfer of ssa allele
RT Streptococcus pyogenes.";
RL Infect. Immun. 64:1161-1165(1996).
DR EMBL; U48793; AAB02149.1; -.
DR HSSP; P34071; 1SE2.
DR PFAM; PF01123; Staph.Strp.toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
SQ SEQUENCE 260 AA; 29836 MW; 3069EA84 CRC32;

Query Match	Similarity	61.3%	Score 1081	DB 2	Length 260
Match Local	Similarity 62.4%		Pred. No. 2,01e-176		
Matches 148	Conservative	38	Mismatches 44	Indels 7	Gaps 6
Db	29	QDDPPEQLNNSQFTGVGNLRCLYDNHNEFGTNVSTGLOLHDLIFPIKDKLKNYD	88		
Oy	3	QDDPPEQLNNSQFTGVGNLRCLYDNHNEFGTNVSTGLOLHDLIFPIKDKLKNYD	62		
Db	89	SVKTFEFSKDLAAKYNKNDVDIFESNYYNICYSE-GN--SCNA-K-KICMGVGYEH	143		
Oy	63	NVREEFKKDLADKKDKYDVDFANAYYYQCYFSKKTNDINSHETDKRKCVMGVTEN	122		
Db	144	RNOIEGRPNITVAVYEDENELISFDITTNKQYVLOELDCTKRIIVSRKNILEFNNSP	203		
Oy	123	GNQLD-KRSTIVRVEDEGKMLLSFDVQTNKKKKTATQELDYLTHNYLVKNNKILEFNNSP	181		
Db	204	YETGYIKFIESSGDSFWYDMPADGALFDOSKYLMLYNDKNTVSSAIAIEVHLTKK	260		
Oy	182	YETGYIKFIESE-NSFWYDMPADGDKFDOSKYLMLYNDKNTVSSAIAIEVHLTKK	237		
RESULT	11	PRELIMINARY:	PRT:	258	AA.
ID	085382				
AC	085382				
DT	01-NOV-1998	(TREMBLrel, 08, Created)			
DT	01-NOV-1998	(TREMBLrel, 08, Last sequence update)			
DT	01-NOV-1999	(TREMBLrel, 12, Last annotation update)			
DE	EXTRACELLULAR ENTEROTOXIN TYPE G PRECURSOR.				
CN	SEC.				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;				
OC	Bacillus/Staphylococcus group; Staphylococcus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-FRI572;				
RX	MEDLINE: 98298056.				
RA	MUNSON S.H., TREMAINE M.T., BETLEY M.J., WELCH R.A.;				
RT	"Identification and characterization of staphylococcal enterotoxin				
RT	types G and I from Staphylococcus aureus."				
RL	Infect. Immun. 66:3337-3348(1998).				
DR	EMBL: AF064773; AAC26660.1; -				
DR	HSSP: P01552; 1SE3.				
DR	PFAM: PF01123; Strep_toxin; 1.				
KM	Signal.				
FT	SIGNAL	1	25	POTENTIAL.	
FT	CHAIN	26	258	ENTEROTOXIN TYPE G.	
SEQ	SEQUENCE	258	AA;	29940	MM; 14DBDEE CRC32;

	Query Match	40.7%	Score 718	DB 2	Length 258
	Best Local Similarity	45.6%	Pred. No. 3,06e-107		
	Matches 110	Conservative	54	Mismatches 65	Indels 12
					Gaps 8
Db	24	NAOAPPKDELINKVSDYKNNKGTMGVNNMLTSPPEVGRGVINSROFSLHDIPEIK-EYK 82			
QY	1	ESQDPKDELHKSSKFT--GLMNNKVLVLDNNHVSAINVKSIDQFLYFLIYSIDTK 57			
Db		83	--SYNEVTELENTLANNYKDKKVDLFGVYFYTCIIPKSEPDIN-ONFGG--CCMYGG 137		
QY	58	LGNYNNVAVEEKNKDLADKYKDYVDGAGANYVQCFESKTKTNDINSHEDTKRKTCMYGG 117			
Db	138	LT-FNNSSENERDKLITVQYOTIDNRQSLGFTTTNNMNTIQELDYKARHWLTREKKLYEF 196			
QY	118	VTEHNGNDLDKRYSTRIVAFPEDKKLLSFQVYQNNKKKTAQELDYLTGRHYLVKKKKLYEEF 177			
Db	197	DGSAAEESGIYKITEKNNTSFWFDELPPKKELVFPVPRKRLNITGDNKVYDSDSIMEVFLN 256			
QY	178	NNSPETGYIKIFIRENEN-SFWYDMAPAG-DKFDOSKYLAMYNNDNNKVDSDKVRKIEVYLT 235			
Db	257	T 257			
QY	236	T 236			

RESULT	12	PRELIMINARY:	PRT:	258 AA.
ID	09ZNF2			
AC	09ZNF2:			
DT	01-MAY-1999	(TREMBLrel, 10, Created)		
DT	01-MAY-1999	(TREMBLrel, 10, Last sequence update)		
DT	01-NOV-1999	(TREMBLrel, 12, Last annotation update)		
DE	ENTEROTOXIN TYPE GV.			
GN	SEG2.			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
OC	Bacillus/Staphylococcus group; Staphylococcus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	ABE J.:			
RT	"Staphylococcal Enterotoxin,"			
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB016487; BAA36693.1; -.			
DR	HSSP; P01552; 1SE3.			
SO	SEQUENCE 258 AA; 29839 MW; 34E42F0F CRC32;			
Query Match	40.3%;	Score 710;	DB 2;	Length 258;
Best Local Similarity	45.2%;	Pred. No. 9,796-106;		
Matches 109;	Conservative	55;	Mismatches 65;	Indels 12; Gaps 9
Db	24	NA00PKIDELKVSADYSKNGKTMGNVLMKSPVEGRVYNSRPLSHDLIPI-EYK	82	
Qy	1	ESQPPDKPELHKSSK-F-T--GLMENKMYLVLDNDHVSAINVKSIDQFLPDLITSIKDK	57	
Db	83	--SYNEVKTELENTLANNYKGGKRVDFGVPEFYTCIIPKSEPDIN--QNFSG--CCMYG	137	
Qy	58	LGNDYNVAREFENKDLADQKXKDYVDGANYVQCYFSKTKNDINSHTDKRKTCMGG	117	
Db	138	LT-FNSSSENEPKLITVOYITDNRQSLGFTTTNNKNMTYIQELDYKANHMLTEKKLYEF	196	
Qy	118	VEHHNGNOIDKRRSTVRFEDGKMILSFEDVOTNKKRYAQLDLDTLRHYLVKNNKLYEF	177	
Db	197	DGSAPESGVIKTEKNTNSFWFMDLPKKKELVPEFYKFNFIYDGNKVVDSKIKMEVPLN	256	
Qy	178	NNSPETETGIKTEINDN-SFWIDMAPRG-DKFDQSKILMTNNDKMKVDSKDVKIEVILT	235	
Db	257	T 257		
Qy	236	T 236		
RESULT	13	PRELIMINARY:	PRT:	236 AA.
ID	Q54696			
AC	Q54696:			

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156;
RX MEDLINE: 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL: X61557; CAA43755.1; -;
DR EMBL: X61556; CAA43754.1; -;
DR EMBL: X61557; CAA43755.1; -;
DR EMBL: X61560; CAA43758.1; -;
Query Match 39.9%; Score 704; DB 2; Length 236;
Best Local Similarity 46.5%; Pred. No. 1.32e-104;
Matches 107; Conservative 53; Mismatches 54; Indels 16; Gaps 8;
Db 22 AQQDPDSQHRSSLVNKL-QNIFYEGDPVTHENKSVQQLSHDLIVNSG--L-NY 77
QY 2 SQDPKPEDELHKSSKFTGLMENMKVLYTDNHNVAINWKSIDQFLYFDLITSIKDTKLGNY 61
Db 78 DKLTELKNEEMATLFFKKNVDIVGEYHYHLYC-----E-NA---KRSACIYGVYTNH 128
QY 62 DNVAVERFNKNDLADKYDVGANGANYCYCSKKTNDINSHTDCKRCKMGVTEH 121
Db 129 EGNHLEIPKILVYKVSIDGQSLSFDIETSKKMTAQOELDYKVKHLLTDNKKQLYTNGPSK 188
QY 122 NGNOLDKYRSTIVAFEDGKMLLSFDVQTNKKKVTQAQELDTLTHRYLVKNNKLYEFNNSP 181
Db 189 YETGYIKFIPKESFNFDFPEP-E-FNQVKYLMYKNDNETLSNTSQI 236
QY 182 YETGYIKFIENEN-SFWYDMMPAPGDFDQSKYLMYNDNKNVDSKDVKI 230
RESULT 14
ID P97163 PRELIMINARY; PRT; 236 AA.
AC P97163; P97164;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS156, AND MGAS500;
RX MEDLINE: 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL: X61556; CAA43754.1; -;
DR EMBL: X61557; CAA43755.1; -;
DR EMBL: X61560; CAA43758.1; -;

DR EMBL: X61555; CAA43753.1; -;
DR EMBL: X61558; CAA43756.1; -;
DR EMBL: X61559; CAA43757.1; -;
DR EMBL: X61554; CAA43752.1; -;
DR HSSP: P01552; 1SE3.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW Signal.
FT NON_TER 1 1
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FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 81A0C2FE CRC32;
Query Match 39.5%; Score 696; DB 2; Length 236;
Best Local Similarity 48.7%; Pred. No. 4.20e-103;
Matches 112; Conservative 43; Mismatches 59; Indels 16; Gaps 9;
Db 22 AQQDPDSQHRSSLVNKL-QNIFYEGDPVTHENKSVQQLSHDLIVNSG--L-NY 77
QY 2 SQDPKPEDELHKSSKFTGLMENMKVLYTDNHNVAINWKSIDQFLYFDLITSIKDTKLGNY 61
Db 78 DKLTELKNEEMATLFFKKNVDIVGEYHYHLYC-----E-NA-E---RSACIYGVYTNH 128
QY 62 DNVAVERFNKNDLADKYDVGANGANYCYCSKKTNDINSHTDCKRCKMGVTEH 121
Db 129 EGNHLEIPKILVYKVSIDGQSLSFDIETSKKMTAQOELDYKVKHLLTDNKKQLYTNGPSK 188
QY 122 NGNOLDKYRSTIVAFEDGKMLLSFDVQTNKKKVTQAQELDTLTHRYLVKNNKLYEFNNSP 181
Db 189 YETGYIKFIPKESFNFDFPEP-E-FNQVKYLMYKNDNETLSNTSQI 236
QY 182 YETGYIKFI-ENENSWYDMMPAPGDFDQSKYLMYNDNKNVDSKDVKI 230
RESULT 15
ID 054779 PRELIMINARY; PRT; 236 AA.
AC 054779; 054613; 054736; 054740; 054741;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE TYPE A EXOTOXIN PRECURSOR (FRAGMENT).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, AND MGAS495;
RX MEDLINE: 92044323.
RA NELSON K., SCHLIEVERT P.M., SELANDER R.K., MUSSER J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL: X61569; CAA43767.1; -;
DR EMBL: X61572; CAA43770.1; -;
DR EMBL: X61568; CAA43766.1; -;
DR EMBL: X61570; CAA43768.1; -;
DR EMBL: X61571; CAA43769.1; -;
DR HSSP: P01552; 1SE3.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PFAM: PF01123; Staph_Strep_toxin; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27468 MW; E902ED6D CRC32;
Query Match 39.4%; Score 694; DB 2; Length 236;

• Sat Apr 22 12:33:42 2000

Best Local Similarity 48.38; Pred. No. 9.98e-103;
Matches 11; Conservative 44; Mismatches 59; Indels 16; Gaps 9;

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Search completed: Thu Apr 20 15:13:37 2000
Job time : 223 secs.

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